

Result No.	Score	Query Match	Length	DB	ID	Description	Summary
1	20	100.0	20	6	C0799984	C0799984 Sequence	
2	20	100.0	21	6	C0799983	C0799983 Sequence	
c 3	19	95.0	19	6	C0799992	C0799992 Sequence	
4	16	80.0	21	6	C0799905	C0799905 Sequence	
5	15	75.0	21	6	C0799906	C0799906 Sequence	
6	14.2	71.0	33	6	AR559501	AR559501 Sequence	
7	14.2	71.0	33	6	AX473165	AX473165 Sequence	
8	13.8	69.0	42	6	AR041097	AR041097 Sequence	
9	13.8	69.0	42	6	AR060705	AR060705 Sequence	
10	13.8	69.0	42	6	AR063138	AR063138 Sequence	
11	13.8	69.0	42	6	AR117027	AR117027 Sequence	
12	13.8	69.0	42	6	164789	164789 Sequence	
13	13.2	66.0	27	6	B41696	E41696 Process for AX499977 Sequence	
14	13.2	66.0	43	6	AX499977	AX499977 Sequence	
15	13.2	66.0	43	6	AX703486	AX703486 Sequence	
16	13.2	66.0	43	6	AX720926	AX720926 Sequence	
17	13.2	66.0	43	6	AX925315	AX925315 Sequence	
18	13.2	66.0	43	6	AX925574	AX925574 Sequence	

ORGANISM	Homo sapiens	Patent: WO 2004030660-A 3 15-APR-2004; The University of British Columbia (CA)
Mammalia; Butheria; Buarchoontoglires; Primates; Catarrhini; Homidae; Homo.		Location/Qualifiers 1. .21
REFERENCE	Gleave, M.E., Rocchi, P. and Sigaevsky, M.	/organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"
AUTHORS		
TITLE	Compositions for treatment of prostate and other cancers	
JOURNAL	The University of British Columbia (CA)	
FEATURES	Location/Qualifiers 1. .21	
source	/organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"	
ORIGIN		
Query Match	100.0%; Score 20; DB 6; Length 21; Best Local Similarity 100.0%; Prod. No. 9.6e+02; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	PAT 28-APR-2004
Qy	1 GGGACGGGGCGTCGGTCAT 20 2 GGAGCGGGCGTCGGTCAT 21	
Db		
RESULT 3		
LOCUS	CQ799992	19 bp RNA
DEFINITION	Sequence 90 from Patent WO2004030660.	
ACCESSION	CQ799992	
VERSION	CQ799992.1	GI:46848939
KEYWORDS		
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
	Mammalia; Butheria; Buarchoontoglires; Primates; Catarrhini; Homidae; Homo.	
REFERENCE	Gleave, M.E., Rocchi, P. and Sigaevsky, M.	/organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"
AUTHORS		
TITLE	Compositions for treatment of prostate and other cancers	
JOURNAL	The University of British Columbia (CA)	
FEATURES	Location/Qualifiers 1. .19	
source	/organism="Homo sapiens" /mol_type="unassigned RNA" /db_xref="taxon:9606"	
ORIGIN		
Query Match	95.0%; Score 19; DB 6; Length 19; Best Local Similarity 100.0%; Prod. No. 2.5e+03; Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	PAT 28-APR-2004
Qy	2 GGACCGGGCGTCGGTCAT 20 Db 19 GGACCGGGCGTCGGTCAT 1	
RESULT 4		
LOCUS	CQ799905	21 bp DNA
DEFINITION	Sequence 3 from Patent WO2004030660.	
ACCESSION	CQ799905	
VERSION	CQ799905.1	GI:46848932
KEYWORDS		
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
	Mammalia; Butheria; Buarchoontoglires; Primates; Catarrhini; Homidae; Homo.	
REFERENCE	Gleave, M.E., Rocchi, P. and Sigaevsky, M.	/organism="ununknown" /mol_type="genomic DNA"
AUTHORS		
TITLE	Compositions for treatment of prostate and other cancers	
ORIGIN		
Query Match	71.0%; Score 14.2; DB 6; Length 33;	

Best Local Similarity 84.2%; Pred. No. 2e+05; Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0; ORIGIN Qy 1 GGGACCCGGGCGCTGGTCA 19 Db 6 GGGTCTCGGGCTCGGGCA 24

ACCESSION AR060705
VERSION AR060705.1
KEYWORDS Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 42)
AUTHORS Plomer, J. Jeffrey, Ryland, J.R., Matthews, M.-A.H., Traylor, D.W., Milne, B.B., Durfee, S.L., Matthews, A.J. and Neway, J.Q.
TITLE Purification of hemoglobin
JOURNAL Patent: US 5840851-A 14 NOV-1998;
FEATURES Location/Qualifiers 1. .42
source /organism="unknown"
/mol_type="unassigned DNA"

RESULT 7
LOCUS AX473165 33 bp DNA
DEFINITION Sequence 16 from Patent WO2303962.
ACCESSION AX473165
VERSION AX473165.1
KEYWORDS SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE Summers, A.O. and Cagniato, J.J.
AUTHORS Met1 binding proteins, recombinant host cells and methods
TITLE Patent: WO 0230962-A 16 APR-2002;
JOURNAL UNIVERSITY OF GEORGIA RESEARCH FOUNDATION, INC. (US)
FEATURES Location/Qualifiers 1. .33
source /organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="primer"

ORIGIN Qy 1 GGGACCCGGGCGCTGGTCA 19
Db 6 GGGTCTCGGGCTCGGGCA 24

ACCESSION AR063138
DEFINITION Sequence 17 from patent US 5844090.
VERSION AR063138
KEYWORDS Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 42)
AUTHORS Anderson, D.C., Matthews, A.J., Trimble, S.P. and Anthony-Cahill, S.
TITLE Modified hemoglobin-like compounds
JOURNAL Patent: US 5844090-A 17 DEC-1998;
FEATURES Location/Qualifiers 1. .42
source /organism="unassigned DNA"

RESULT 8
LOCUS AR041097 42 bp DNA
DEFINITION Sequence 21 from patent US 5811264.
ACCESSION AR041097
VERSION AR041097.1
KEYWORDS SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 42)
AUTHORS Aitken, J.F., Apostol, T.Z., Lippincott, J.A. and Levine, J.D.
TITLE Proteins with mutations to decrease N-terminal methylation
JOURNAL Patent: US 5811264-A 21 SEP-1998;
FEATURES Location/Qualifiers 1. .42
source /organism="unknown"
/mol_type="unassigned DNA"

ORIGIN Qy 1 GGGACCCGGGCGCTGGTCA 20
Db 16 ACGGGGCTCGGGCTCGGTGT 32

ACCESSION AR117027
DEFINITION Sequence 21 from patent US 6140071.
VERSION AR117027
KEYWORDS Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 42)
AUTHORS Aitken, J.F., Apostol, T.Z., Lippincott, J.A. and Levine, J.D.
TITLE Proteins with mutations to decrease N-terminal methylation
JOURNAL Patent: US 6140071-A 21 OCT-2000;
FEATURES Location/Qualifiers 1. .42
source /organism="unknown"
/mol_type="unassigned DNA"

RESULT 9
LOCUS AR060705 42 bp DNA
DEFINITION Sequence 14 from patent US 5840851.

ORIGIN /mol_type="genomic DNA"
 /db_xref="taxon:32630"

Query Match 69.0%; Score 13.8; DB 6; Length 42;
 Best Local Similarity 89.2%; Pred. No 2.8e+05;
 Matches 15; Conservative 0; Mismatches 2;
 Indels 0; Gaps 0;

Qy 4 ACGGCGCTCGGTAT 20
 ||||| ||||| |||||
 Db 16 ACGGCTGGCTCGGTCT 32
 ||||| ||||| |||||

RESULT 12
 I64789 164789 42 bp DNA linear PAT 07-OCT-1997
 LOCUS Sequence 14 from patent US 5665869.
 DEFINITION
 ACCESSION I64789
 VERSION 164789.1 GI:2481683
 KEYWORDS Unknown.
 SOURCE
 ORGANISM Unclassified.
 REFERENCES 1 (bases 1 to 42)
 Ryland, J.R., Matthew, M.-A.H., Ernst, U.P., Houk, D.B., Traylor, D.W.
 and Williams, L.R.
 TITLE Method for the rapid removal of protoporphyrin from protoporphyrin
 IX-containing solutions of hemoglobin
 JOURNAL Patent: US 5665869-A 14 09-SEP-1997;
 FEATURES Location/Qualifiers 1. .42
 /organism="unknown"
 /mol_type="unassigned DNA"
 SOURCE
 ORIGIN

Query Match 69.0%; Score 13.8; DB 6; Length 42;
 Best Local Similarity 89.2%; Pred. No 2.8e+05;
 Matches 15; Conservative 0; Mismatches 2;
 Indels 0; Gaps 0;

Qy 4 ACGGCGCTCGGTAT 20
 ||||| ||||| |||||
 Db 16 ACGGCTGGCTCGGTCT 32
 ||||| ||||| |||||

RESULT 13
 E41696 E41696 27 bp DNA linear PAT 31-JAN-2002
 LOCUS Process for producing L-glutamic acid by fermentation.
 DEFINITION
 ACCESSION E41696
 VERSION E41696.1 GI:186333367
 KEYWORDS JP 2001069979-A/13.
 ORGANISM Synthetic construct
 OTHER SEQUENCES: Artificial sequences.
 REFERENCES 1 (bases 1 to 27)
 Fujii, M. and Imanaka, T.
 TITLE Process for producing L-glutamic acid by fermentation
 JOURNAL Patent: JP 2001069979-A 13 21-MAR-2001;
 JAPAN TOBACCO INC, TADAYUKI IMANAKA
 COMMENT OS Artificial Sequence
 PN JP 2001069979-A/13
 PD 21-MAR-2001
 PP 31-AUG-1999 JP 1999245121
 PI MIKIO FUJII, TADAYUKI IMANAKA
 PC C12N15/09, C12N1/21, C12P13/14 // (C12N1/21, C12R1:15), (C12P13/14,
 C12R1:15),
 PC C12N15/00
 CC
 FH Key
 FT Source 1. .27
 /organism="Artificial Sequence".
 FEATURES Source
 /organism="Artificial construct".
 ORIGIN Query Match 66.0%; Score 13.2; DB 6;
 Best Local Similarity 83.3%; Pred. No. 4.9e+05;
 Matches 3; Conservative 0; Mismatches 3;
 Indels 0; Gaps 0;

ORIGIN /mol_type="genomic DNA"
 /db_xref="taxon:32630"

Query Match 66.0%; Score 13.2; DB 6;
 Best Local Similarity 83.3%; Pred. No. 5.2e+05;
 Matches 15; Conservative 0; Mismatches 3;
 Indels 0; Gaps 0;

Qy 3 GACGGCGCTCGGTAT 20
 ||||| ||||| |||||
 Db 9 GACGGCGAAACGGCCAT 26
 ||||| |||||

RESULT 14
 AX496977 43 bp DNA linear PAT 26-SEP-2002
 LOCUS Sequence 48 from Patent WO0228286.
 DEFINITION AX496977
 ACCESSION AX496977
 VERSION AX496977.1 GI:23342420
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.
 REFERENCES 1
 Li, M., Melander, C. and Liu, H.,
 /organism="Homo sapiens"
 Methods and compositions for the construction and use of fusion
 libraries
 JOURNAL Patent: WO 0228286-A 48 21-MAR-2002;
 Xencor, Inc. (US)
 FEATURES Location/Qualifiers 1. .43
 SOURCE /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

ORIGIN

Query Match 66.0%; Score 13.2; DB 6;
 Best Local Similarity 83.3%; Pred. No. 4.9e+05;
 Matches 15; Conservative 0; Mismatches 3;
 Indels 0; Gaps 0;

Qy 1 GGGACGGGGCGCTCGGTCT 18
 ||||| ||||| ||||| |||||
 Db 8 GGGGCTCGGCGTCGTC 25
 ||||| ||||| |||||

RESULT 15
 AX703486 43 bp DNA linear PAT 03-APR-2003
 LOCUS Sequence 48 from Patent WO020666653.
 DEFINITION AX703486
 ACCESSION AX703486
 VERSION AX703486.1 GI:29538451
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.
 REFERENCES 1
 Li, M. and Liu, Y.C.,
 Prokaryotic libraries and uses
 JOURNAL Patent: WO 02066653-A 48 29-AUG-2002;
 Xencor (US)
 FEATURES Location/Qualifiers 1. .43
 SOURCE /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

ORIGIN Query Match 66.0%; Score 13.2; DB 6;
 Best Local Similarity 83.3%; Pred. No. 4.9e+05;
 Matches 3; Conservative 0; Mismatches 3;
 Indels 0; Gaps 0;

	Matches	15;	Conservative	0;	Mismatches	3;	Indels	0;	Gaps	0;
Qy	1	GGGACCGGGCGCTCGTC	18							
Db	8	GGGCTGGCGCTCGTC	25							

Search completed: December 13, 2005, 13:58:20
Job time : 1701 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using bw model
Run on: December 13, 2005, 08:34:39 ; Search time 260 Seconds
(without alignments)
512.669 Million cell updates/sec

Title: US-10-605-498-82
Perfect score: 20
Sequence: 1 ggacgcggcgctggat 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 4879314

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing First 45 summaries

Database : N_Geneseq_21:*

1: geneseqn1980s:*

2: geneseqn1990s:*

3: geneseqn2000s:*

4: geneseqn2001as:*

5: geneseqn2001bs:*

6: geneseqn2002as:*

7: geneseqn2002bs:*

8: geneseqn2003as:*

9: geneseqn2003bs:*

10: geneseqn2003cs:*

11: geneseqn2003ds:*

12: geneseqn2004as:*

13: geneseqn2004bs:*

14: geneseqn2005s:*

20 13.2 66.0 43 6 AAD46152 Rep68 and
21 13.2 66.0 43 6 AAD44614 Rep 68 an
22 13.2 66.0 43 8 ACC69559 Rep68 and
23 13.2 66.0 43 10 ABX96683 Rep68 and
24 13.2 66.0 43 10 ABX96538 Rep68 and
25 13.2 66.0 43 10 ABX95302 Neisseria
c 26 13.2 66.0 44 3 AAZ55402
c 27 13.2 66.0 49 2 AAT80499 Hepatoma
c 28 12.8 64.0 21 2 AAV51704 Sea mays
c 29 12.8 64.0 23 3 AAA75395
c 30 12.8 64.0 24 8 ABZ5873 Zebrafish
c 31 12.8 64.0 25 9 ACT84537 Human mic
c 32 12.8 64.0 29 12 ADO31537 Human CFT
c 33 12.8 64.0 30 14 ADY0845 PCR fragm
c 34 12.8 64.0 37 2 AAX55824 PCR prime
c 35 12.8 64.0 39 6 ABA98226 Oligonucle
c 36 12.8 64.0 40 2 AAT69484 Plasmid P
c 37 12.8 64.0 40 2 AAT69525 Plasmid P
c 38 12.8 64.0 40 2 AAV51220 Maize Pol
c 39 12.8 64.0 40 2 AAX88908 Circular
c 40 12.8 64.0 40 2 AAX88950 Circular
c 41 12.8 64.0 40 6 ABA98183 Oligonucle
c 42 12.8 64.0 40 6 ABA98184 Oligonucle
c 43 12.8 64.0 41 6 ABV75699 Human zin
c 44 12.8 64.0 42 14 AEB08695 RSV-X low
c 45 12.8 64.0 44 14 AEB08694 RSV-X low

ALIGNMENTS

RESULT 1
ADM94732
ID ADM94732 standard; DNA; 20 BP.
XX
ADM94732;
AC
XX
DT 01-JUL-2004 (first entry)
XX
DB Human heat shock protein 27 antisense oligonucleotide SEQ ID NO:82.
XX
heat shock protein 27; hsp27; cyrostatic; gene therapy;
heat shock protein 27 inhibitor; hsp27 inhibitor; cancer; human;
antisense oligonucleotide; ss.
XX
Homo sapiens.
OS
Synthetic.
XX
WO2004030660-A2.
XX
15-APR-2004.
PD
XX
PP 02-OCT-2003; 2003WO-CA001588.
XX
PR 02-OCT-2002; 2002US-0415859P.
PR 18-APR-2003; 2003US-0463952P.
XX
(UTPR-) UNIV BRITISH COLUMBIA.
PA
XX
PI Gleave ME, Rocchi P, Signaevsky M;
XX
DR WPI: 2004-316331/29.
XX
PT New composition comprising a therapeutic agent that reduces the amount of
active hsp27 in hsp27 expressing cells exposed to the therapeutic agent,
useful in treating cancer, e.g., prostate cancer or a central nervous
system malignancy.
XX
PS Claim 6; SEQ ID NO 82; 38pp; English.
XX
CC The present invention describes a composition which comprises a
therapeutic agent that reduces the amount of active heat shock protein 27
(hsp27) in hsp27 expressing cells exposed to the therapeutic agent. The
CC

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	12 ADM94732	ADM94732 Human hea
2	20	100.0	21	12 ADM94731	ADM94731 Human hea
c 3	19	95.0	19	12 ADM94740	ADM94740 Human hea
c 4	16	80.0	21	12 ADM94653	ADM94653 Human hea
5	15	75.0	21	12 ADM94654	ADM94654 Human hea
6	14.2	71.0	33	6 ABK52211	ABK52211 Synthetic
c 7	14.2	71.0	47	8 ABZ68938	ABZ68938 PCR prime
8	13	14	25	9 ACH58106	ACH58106 DNA large
9	13	8	69	2 AAQ87144	AAQ87144 PBR322 Or
10	13	8	69	2 ART3275	ART3275 Oligo TG6
11	13	8	69	2 AAT73265	AAT73265 Downstrea
12	13	8	69	2 AAT60986	AAT60986 Downstrea
13	13	8	69	2 AAV58346	AAV58346 Primer TG
14	13	8	69	5 AAC81485	AAC81485 PBR322 Or
c 15	13	2	66	9 ACT103862	ACT103862 Human mic
16	13	2	66	9 ACI65798	ACI65798 Human mic
17	13	2	66	9 AAH21740	AAH21740 Corynebac
18	13	2	66	4 AAA91324	AAA91324 Rep68 and
19	13	2	66	6 ADD36295	ADD36295 Rep68 and

CC composition has cytostatic activity, and can be used in gene therapy. The CC composition is useful in treating cancer, e.g., prostate, bladder, lung, CC breast, pancreatic, colon, skin (for example melanoma), renal or ovarian CC cancer or a central nervous system malignancy. The present sequence CC represents a human hsp27 antisense oligonucleotide which is used in the CC exemplification of the present invention.

XX Sequence 20 BP; 2 A; 6 C; 9 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 12; Length 20;

Best Local Similarity 100.0%; Pred. No. 12;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGACGGGGCTCGGTAT 20

Db 1 GGGACGGGGCTCGGTAT 20

Sequence 20 BP; 2 A; 6 C; 9 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 12; Length 20;

Best Local Similarity 100.0%; Pred. No. 12;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGACGGGGCTCGGTAT 20

Db 1 GGGACGGGGCTCGGTAT 20

Sequence 20 BP; 2 A; 6 C; 9 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 12; Length 21;

Best Local Similarity 100.0%; Pred. No. 12;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGACGGGGCTCGGTAT 20

Db 1 GGGACGGGGCTCGGTAT 20

Sequence 21 BP; 2 A; 6 C; 10 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 12; Length 21;

Best Local Similarity 100.0%; Pred. No. 12;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGACGGGGCTCGGTAT 20

Db 1 GGGACGGGGCTCGGTAT 20

Sequence 21 BP; 2 A; 6 C; 10 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 12; Length 21;

Best Local Similarity 100.0%; Pred. No. 12;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGACGGGGCTCGGTAT 20

Db 1 GGGACGGGGCTCGGTAT 20

Sequence 21 BP; 2 A; 6 C; 10 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 12; Length 21;

Best Local Similarity 100.0%; Pred. No. 12;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGACGGGGCTCGGTAT 20

Db 1 GGGACGGGGCTCGGTAT 20

Sequence 21 BP; 2 A; 6 C; 10 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 12; Length 21;

Best Local Similarity 100.0%; Pred. No. 12;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGACGGGGCTCGGTAT 20

Db 1 GGGACGGGGCTCGGTAT 20

Sequence 21 BP; 2 A; 6 C; 10 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 12; Length 21;

Best Local Similarity 100.0%; Pred. No. 12;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGACGGGGCTCGGTAT 20

Db 1 GGGACGGGGCTCGGTAT 20

Sequence 21 BP; 2 A; 6 C; 10 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 12; Length 21;

Best Local Similarity 100.0%; Pred. No. 12;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGACGGGGCTCGGTAT 20

Db 1 GGGACGGGGCTCGGTAT 20

RESULT 2
ID ADM94731 standard; DNA; 21 BP.
XX AC ADM94731;
XX DT 01-JUL-2004 (first entry)

DE Human heat shock protein 27 antisense oligonucleotide SEQ ID NO:81.
XX KW heat shock protein 27; hsp27; cytostatic; gene therapy;
KW heat shock protein 27 inhibitor; hsp27 inhibitor; cancer; human;
KW antisense oligonucleotide; ss.

OS Homo sapiens.
OS Synthetic.
XX PN WO2004030660-A2.

XX PD 15-APR-2004.
XX DE 02-OCT-2003; 2003WO-CA001588.

XX PR 02-OCT-2002; 2002US-0415859P.
XX PR 18-APR-2003; 2003US-0463952P.

XX PA (UYBR-) UNIV BRITISH COLUMBIA.
XX PI Gleave ME, Rocchi P, Sigmaevsky M;
XX DR; 2004-316331/29.

XX New composition comprising a therapeutic agent that reduces the amount of active hsp27 in hsp27 expressing cells exposed to the therapeutic agent, PT useful in treating cancer, e.g., prostate, bladder, lung, PT system malignancy.

XX PA (UYBR-) UNIV BRITISH COLUMBIA.
XX The present invention describes a composition which comprises a CC therapeutic agent that reduces the amount of active heat shock protein 27 CC (hsp27) in hsp27 expressing cells exposed to the therapeutic agent. The CC composition has cytostatic activity, and can be used in gene therapy. The CC composition is useful in treating cancer, e.g., prostate, bladder, lung, CC breast, pancreatic, colon, skin (for example melanoma), renal or ovarian CC cancer or a central nervous system malignancy. The present sequence CC represents a human hsp27 short interfering RNA (siRNA) oligonucleotide CC which is used in the exemplification of the present invention.

XX SQ Sequence 19 BP; 3 A; 8 C; 6 G; 0 T; 2 U; 0 Other;

XX Query Match 95.0%; Score 19; DB 12; Length 19;
Best Local Similarity 100.0%; Pred. No. 34;

CC Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGACGGGGCTCGGTAT 20
Db 1 GGGACGGGGCTCGGTAT 20

RESULT 3
ID ADM94740/C
XX AC ADM94740 standard; DNA; 19 BP.
XX DT 01-JUL-2004 (first entry)

DE Human heat shock protein 27 siRNA oligonucleotide SEQ ID NO:90.
XX KW heat shock protein 27; hsp27; cytostatic; gene therapy;
KW heat shock protein 27 inhibitor; hsp27 inhibitor; cancer; human;
KW short interfering RNA; siRNA; RNA interference; RNAi; ds.

OS Homo sapiens.
OS Synthetic.
XX PN WO2004030660-A2.

XX PD 15-APR-2004.
XX DE 02-OCT-2003; 2003WO-CA001588.

XX PR 02-OCT-2002; 2002US-0415859P.
XX PR 18-APR-2003; 2003US-0463952P.

XX PA (UYBR-) UNIV BRITISH COLUMBIA.
XX The present invention describes a composition which comprises a CC therapeutic agent that reduces the amount of active heat shock protein 27 CC (hsp27) in hsp27 expressing cells exposed to the therapeutic agent. The CC composition has cytostatic activity, and can be used in gene therapy. The CC composition is useful in treating cancer, e.g., prostate, bladder, lung, CC breast, pancreatic, colon, skin (for example melanoma), renal or ovarian CC cancer or a central nervous system malignancy. The present sequence CC represents a human hsp27 short interfering RNA (siRNA) oligonucleotide CC which is used in the exemplification of the present invention.

XX SQ Sequence 19 BP; 3 A; 8 C; 6 G; 0 T; 2 U; 0 Other;

XX Query Match 95.0%; Score 19; DB 12; Length 19;
Best Local Similarity 100.0%; Pred. No. 34;

CC Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGACGGGGCTCGGTAT 20
Db 1 GGGACGGGGCTCGGTAT 20

RESULT 4
ID ADM94653
XX AC ADM94653 standard; DNA; 21 BP.
XX DT 01-JUL-2004 (first entry)

DE Human heat shock protein 27 siRNA oligonucleotide SEQ ID NO:91.
XX KW heat shock protein 27; hsp27; cytostatic; gene therapy;
KW heat shock protein 27 inhibitor; hsp27 inhibitor; cancer; human;
KW short interfering RNA; siRNA; RNA interference; RNAi; ds.

OS Homo sapiens.
OS Synthetic.
XX PN WO2004030660-A2.

XX PD 15-APR-2004.
XX DE 02-OCT-2003; 2003WO-CA001588.

XX PR 02-OCT-2002; 2002US-0415859P.
XX PR 18-APR-2003; 2003US-0463952P.

XX PA (UYBR-) UNIV BRITISH COLUMBIA.
XX The present invention describes a composition which comprises a CC therapeutic agent that reduces the amount of active heat shock protein 27 CC (hsp27) in hsp27 expressing cells exposed to the therapeutic agent. The CC composition has cytostatic activity, and can be used in gene therapy. The CC composition is useful in treating cancer, e.g., prostate, bladder, lung, CC breast, pancreatic, colon, skin (for example melanoma), renal or ovarian CC cancer or a central nervous system malignancy. The present sequence CC represents a human hsp27 antisense oligonucleotide which is used in the CC exemplification of the present invention.

Human heat shock protein 27 antisense oligonucleotide SEQ ID NO:3.
 XX heat shock protein 27; hsp27; cytosstatic; gene therapy;
 XX heat shock protein 27 inhibitor; hsp27 inhibitor; cancer; human;
 XX antisense oligonucleotide; ss.
 OS Homo sapiens.
 OS Synthetic.
 XX WO2004030660-A2.
 XX PD 15-APR-2004.
 XX PR 02-OCT-2003; 2003WO-CA001588.
 XX PR 02-OCT-2003; 2003WO-CA001588.
 XX PR 02-OCT-2002; 2002US-0415859P.
 XX PR 18-APR-2003; 2003US-0463952P.
 XX PA (UYBR-) UNIV BRITISH COLUMBIA.
 XX WPI; 2004-316331/29.
 XX PCT New composition comprising a therapeutic agent that reduces the amount of active hsp27 in hsp27 expressing cells exposed to the therapeutic agent, e.g., prostate cancer or a central nervous system malignancy.
 XX PCT New composition comprising a therapeutic agent that reduces the amount of active hsp27 in hsp27 expressing cells exposed to the therapeutic agent, e.g., prostate cancer or a central nervous system malignancy. The present sequence represents a human hsp27 antisense oligonucleotide which is used in the exemplification of the present invention.
 XX PCT Claim 5; SEQ ID NO 4; 38pp; English.
 XX PCT The present invention describes a composition which comprises a therapeutic agent that reduces the amount of active heat shock protein 27 (hsp27) in hsp27 expressing cells exposed to the therapeutic agent. The composition has cytostatic activity, and can be used in gene therapy. The composition is useful in treating cancer, e.g., prostate, bladder, lung, breast, pancreatic, colon, skin (for example melanoma), renal or ovarian cancer or a central nervous system malignancy. The present sequence represents a human hsp27 antisense oligonucleotide which is used in the exemplification of the present invention.
 XX SQ Sequence 21 BP; 4 A; 5 C; 11 G; 1 T; 0 U; 0 Other;
 XX SQ Query Match 75.0%; Score 15; DB 12; Length 21;
 XX Best Local Similarity 100.0%; Pred. No. 2.4e+03;
 XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0
 XX Qy 1 CGGAGCGGGCGGCGTCG 15
 XX Db 7 GGGAGCGGGCGGCGTCG 21
 XX PCT RESULT 6
 XX ABK52211 ID ABK52211 Standard; DNA; 33 BP.
 XX ABK52211 XX
 XX AC AC
 XX DT 13-AUG-2002 (first entry)
 XX DE Synthetic product 2 reverse PCR primer for construction of pASK-MBD.
 XX KW Mercuric ion; contaminated soil; ground water; hydroponic solution;
 XX KW irrigation water; waste stream; contaminated aqueous medium;
 XX KW biological fluid; Gastrointestinal tract; chelon protein;
 XX KW enteric bacteria; toxic metal ion; mercury; cadmium; divalent cation;
 XX KW heavy metal binding protein; pASK-MBD; PCR; primer; ss.
 XX OS Synthetic.
 XX PN WO200230962-A2.
 XX PD 18-APR-2002.
 XX PR 12-OCT-2001; 2001WO-US031819.
 XX PR 12-OCT-2000; 2000US-0240465P.
 XX PA (UYGE-) UNIV GEORGIA RES FOUND INC.
 XX PI Summers AO, Caguat JJ;
 XX DR WPI; 2002-435437/46.
 XX PCT Novel non-naturally occurring recombinant DNA molecule encoding a chelon protein useful for binding divalent cation mercury from contaminated
 XX PCT protein.

PT soil, water, aqueous medium including biological fluids.
 PS Disclosure: Page 24; 42pp; English.

XX The present invention relates to a new non-naturally occurring recombinant DNA molecule comprising a sequence encoding a chelon protein which binds mercuric ions. The invention is useful for recombinantly producing a protein in a host-cell, by infecting or transforming a host cell capable of expressing a chelon coding sequence with a vector comprising a promoter active in the host cell operably linked to a coding region for the protein to produce a recombinant host cell and culturing the recombinant host cell under conditions where DNA is expressed. The nucleic acid encoding the chelon protein is useful for binding divalent mercuric ions, to take up, sequester and concentrate the heavy metal ions from contaminated soil, ground water, hydroponic solutions or irrigation water of waste streams. The DNA of the invention, when immobilised onto a solid support, is useful for concentrating heavy metal ions from contaminated environment waste streams or contaminated aqueous medium including biological fluids. The nucleic acid, when recombinantly expressed in enteric bacteria (which are nontoxicogenic and nonpathogenicic), is suitable for use in the in vivo sequestration and elimination of mercuric ion from gastrointestinal tracts of animals or humans exposed to toxic metal ions such as mercury and/or cadmium. The molecules of the invention are also useful in water treatment resins. The nucleic acid of the invention is highly specific and binds divalent ratios such as mercury or cadmium with high affinity. The present nucleic acid sequence represents synthetic product 2 reverse PCR primer that was used in the methods of the invention for construction of PASK-MBD vector

XX Sequence 33 BP; 6 A; 8 C; 12 G; 7 T; 0 U; 0 Other;

Query Match 71.0%; Score 14.2; DB 6; Length 33;
 Best Local Similarity 84.2%; Pred. No. 5.4e+03;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 GGGAGGGGGGGGGGGTCA 19
 Db 6 GGGTCTCGGGGGGGGA 24

RESULT 7
 AB268928/C
 ID ABZ68928 Standard; DNA; 47 BP.
 XX AC ABZ68928;
 XX DT 28-MAY-2003 (first entry)
 XX DE PCR primer used to amplify a PKS domain DNA sequence.
 XX KW Simvastatin; polyketide synthase; PKS; HMPKSB2; PCR; primer; ss.
 XX Unidentified.
 OS WO2003010324-A2.
 XX PN 2002US-00215112.
 XX PR 08-AUG-2001; 2001US-0311040P.
 XX DE (MITT) MITTMANN M.
 XX PI Mittmann M;
 XX WPI; 2003-576608/54.

XX The present invention relates to nucleic acid sequences that are complementary to particular genes, and can be used as probes for a variety of analyses such as gene expression analysis. Each probe comprises 9 or more consecutive nucleotides from at least one of 14936 nucleotide sequences defined in the patent, or their perfect sense match, sense mismatch, antisense match or antisense mismatch oligonucleotides. The probes may be used in an array comprising at least 10 distinct nucleic acid probes. The array is useful in monitoring gene expression levels by hybridisation to a DNA library, in analysing genetic variations, and in hybridising tag-labelled compounds. The probes are useful for identifying family members of a gene. The probes are also useful in in situ hybridisations, in screening cDNA or genomic libraries (or derived subclones) for additional clones containing segments of DNA

XX PT preparing simvastatin or its analogs or derivatives, by providing a host having a customized gene encoding a polyketide synthase, and fermenting the host to obtain simvastatin or its analogs or derivatives.
 XX PR Example 1.2.3; Page 21; 40pp; English.
 XX PS

XX The specification describes a method of preparing simvastatin or its analogues or derivatives by biological expression. The method comprises providing a host having a customized gene encoding for a polyketide synthase (PKS), and fermenting the host to obtain simvastatin or its analogues or derivatives. The method is useful for producing simvastatin or its analogs or derivatives. PCR primers AB68927-28 were used to amplify a PKS domain DNA sequence. The amplified fragment was used in the construction of the hybrid modular PKS B2 (HMPKSB2), for use in the method of the invention

XX Sequence 47 BP; 8 A; 14 C; 20 G; 5 T; 0 U; 0 Other;

Query Match 71.0%; Score 14.2; DB 8; Length 47;
 Best Local Similarity 84.2%; Pred. No. 5.4e+03;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 GGGAGGGGGGGGGTCA 19
 Db 33 GGGCGGGGGGGTCA 15

RESULT 8
 ACH58106
 ID ACH58106 Standard; DNA; 25 BP.
 XX AC ACH58106;
 XX DT 16-OCT-2003 (first entry)
 XX DE DNA target sequence #7242 useful in array for genetic analyses.
 XX KW Gene expression analysis; array; hybridisation; genetic variation; tag-labelled compound; gene family; in situ hybridisation; library screening; southern hybridisation; northern hybridisation; dot-blot hybridisation; gene sequence; mutation detection;
 XX KW target sequence; probe; PCR; primer; ss.
 OS Unidentified.
 XX US2003082596-A1.
 XX PN 2002US-00215112.
 XX PR 01-MAY-2003.
 XX WPI; 2003-576608/54.

XX The present invention relates to nucleic acid sequences that are complementary to particular genes, and can be used as probes for a variety of analyses such as gene expression analysis. Each probe comprises 9 or more consecutive nucleotides from at least one of 14936 nucleotide sequences defined in the patent, or their perfect sense match, sense mismatch, antisense match or antisense mismatch oligonucleotides. The probes may be used in an array comprising at least 10 distinct nucleic acid probes. The array is useful in monitoring gene expression levels by hybridisation to a DNA library, in analysing genetic variations, and in hybridising tag-labelled compounds. The probes are useful for identifying family members of a gene. The probes are also useful in in situ hybridisations, in screening cDNA or genomic libraries (or derived subclones) for additional clones containing segments of DNA

XX PT preparing simvastatin or its analogs or derivatives, by providing a host having a customized gene encoding a polyketide synthase, and fermenting the host to obtain simvastatin or its analogs or derivatives.
 XX PR Example 1.2.3; Page 21; 40pp; English.
 XX PS

CC that have been previously isolated and sequenced, in southern, northern, or dot-blot hybridisation of genomic DNA to identify or detect the sequence of any gene or detect specific mutations in any gene, and in mapping the 5' termini of mRNA molecules by primer extensions. The nucleic acid sequences of the invention are also useful as PCR primers. The invention provides a large collection of nucleic acid sequences complementary to particular genes with a wide range of analytical uses. ACH0865-ACH65260 represent the target sequences of the invention. Note: The sequence data for this patent was obtained in electronic format directly from the USPTO web site at seqdata.uspto.gov/patsidentry.html

SQ Sequence 25 BP; 4 A; 9 C; 9 G; 3 T; 0 U; 0 Other;

Query Match 70.0%; Score 14; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 6.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GGACGGCCGCTCG 15
Db 2 GGACGGCCGCTCG 15

RESULT 9
AAQ87144

ID AAQ87144 standard; DNA; 42 BP.

XX AAQ87144;

AC XX;

DT 24-JAN-1996 (first entry)

XX pBR322 ori downstream amplification primer TG63.

XX Primer; PCR; amplification; recombinant haemoglobin; alpha subunit;

KW expression vector; purity; beta subunit; tac promoter; tet gene;

KW lambda repressor gene; lacI; ss.

XX Synthetic.

XX PN WO9514038-A2.

XX PD 26-MAY-1995.

XX PP 15-NOV-1994; 94WO-US013034.

XX PR 15-NOV-1993; 93US-00153071.

XX (SOMA-) SOMATOGEN INC.

XX Milne EB, Plomer JJ, Rausch SK, Hodgenson DC, Ryland JR;

XX Matthews MH, Ernst UP, Houk DE, Taylor DW, Williams LR;

XX Mitchell DJ, Chivers ML, Belval TK;

XX DR 1995-200344/26.

XX Purification of haemoglobin, esp. recombinant haemoglobin - using e.g.

PT immobilised metal affinity chromatography heating steps, anion exchange

PT resins and chelating agents.

XX Example 1; Page 31; 77pp; English.

XX The primers AAQ87135-50 were used to subclone the haemoglobin alpha and beta genes into bacterial expression vectors. The vectors thus constructed were used in methods to produce recombinant haemoglobin which can be purified to pharmaceutically acceptable levels of purity by the methods of the specification. This primer binds downstream of the pBR322 origin of replication (ori) at pos. 2380-2404. The primer with primer TG62 (AAQ87143) is used to amplify the pBR322 ori. The ori is used in the construction of the expression vector pSGE705. This vector contains two copies of the haemoglobin alpha subunit gene in tandem, linked to the beta gene, all under control of the tac promoter (AAQ87136-). The plasmid also has inserted the tet gene and the lacI gene for regulation of the production of haemoglobin

SQ Sequence 42 BP; 3 A; 12 C; 16 G; 11 T; 0 U; 0 Other;

Query Match 69.0%; Score 13.8; DB 2;

Best Local Similarity 88.2%; Pred. No. 8.3e+03;

Matches 15; Conservative 0; Mismatches 2;

Indels 0; Gaps 0;

Qy 4 ACGGCGCTGGCAT 20
16 ACGTGCGCTGGT 32

Db

RESULT 10
AAV32725

ID AAV32725 standard; DNA; 42 BP.

XX XX

AC AAV32725;

XX DT 07-JAN-1997 (first entry)

XX DE Oligo TG63 for creation of recombinant haemoglobin.

XX KW Haemoglobin; alpha globin; beta globin; Hb; dietary supplement; anaemia;

XX molecular weight marker; oxygen carrier; transfusion; oxygen delivery;

XX erythrocyte; nitric oxide; non-oxygenated ligand; therapy; hypertension;

XX hypotension; septic shock; polymerase chain reaction; primer; amplify;

XX PCR; ss.

XX OS Synthetic.

XX XX

XX PN WO9615151-A1.

XX XX

XX PD 23-MAY-1996.

XX XX

XX PP 11-MAY-1995;

XX XX

XX PR 14-NOV-1994; 94US-00339304.

XX PR 10-MAY-1995;

XX XX

XX PA (SOMA-) SOMATOGEN INC.

XX XX

XX PI Plomer JJ, Ryland JR, Matthews MH, Taylor DW, Milne EE;

XX PI Durfee SL, Matthews AJ, Neway JO;

XX XX

XX DR 1996-259784/26.

XX XX

XX PT Purifich. of haemoglobin soln. from cell lysate by metal affinity

XX chromatography - opt. followed by anion exchange chromatography and

XX oxygenation of the soln., partic. useful as therapeutic oxygen carrier.

XX XX

XX PS Example 1; Page 30; 74pp; English.

XX XX

XX CC AAV32717-T32725 represent oligonucleotides used in the creation of the

CC plasmid pSGE705. This sequence represents the downstream primer for the

CC pBR322 ori. pSGE705 contains the pBR322 ori, a lacI gene, a di-alpha

CC globin gene, a tetracycline resistance gene, and a beta globin gene. A

CC lysate of bacteria transformed with pSGE705 is then used in the method of

CC the invention for production of a haemoglobin (Hb) solution. In the

CC method, a Hb-containing lysate is applied to an immobile metal

CC affinity chromatography resin loaded with a divalent ion. The resin is

CC washed with a solution containing a competitive ligand, then washed with

CC a buffer to remove the competitive ligand. The solution is the eluted to

CC recover a partially purified Hb solution. The Hb solution produced can be

CC used as dietary supplements to provide iron, as molecular weight markers,

CC and as oxygen carriers for transfusions. Also, the solution can be used

CC to treat anaemia, to deliver oxygen to cell cultures or, in vivo, to

CC tissues downstream of occlusions that cannot be reached by erythrocytes.

CC The Hb can also function to deliver or remove nitric oxide (NO) or non-

CC oxygenated ligands, as a drug delivery vehicle, and to remove oxygen from

CC solutions. The delivery of NO is useful as therapy in cases of

CC hypotension, while removal of excess NO can be used to treat erythrocytes,

CC and septic shock. The method can be applied to lysates of erythrocytes,

CC or of recombinant cells, and is able to remove the large amounts of

CC contaminants present in recombinant Hb solutions

XX
 PF 29-FBB-1996; 96US-00609271.
 XX
 PR 27-JAN-1994; 94US-00188374.
 XX
 PA (SOMA-) SOMATOGEN INC.
 Levine JD, Aitken JF, Apostol IZ, Lippincott JA;
 PI
 WPI; 1998-530871/45.
 XX
 Mutated protein without proline at position 4 - to eliminate N-terminal
 PT methylation.
 XX
 Example 1; Col 15; 26pp; English.
 XX
 This sequence represents a primer for a mutated haemoglobin of the
 CC invention. The invention relates to a mutated variant of a protein that
 CC has proline at position 4 and is at least partially methylated on its N-
 CC terminus when expressed in bacteria, the variant has an amino acid other
 CC than proline at position 4 and is not methylated on its N-terminus when
 CC expressed in bacteria. Recombinant haemoglobin that is not N-terminally
 CC methylated might avoid the immunological consequences implied by such
 CC methylation.
 XX
 Sequence 42 BP; 3 A; 12 C; 16 G; 11 T; 0 U; 0 Other;
 SQ
 Query Match 69.0%; Score 13.8%; DB 2; Length 42;
 Best Local Similarity 88.2%; Pred. No. 8.3e+03;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 4 ACGGCGCGCTGGTCA 20
 Db 16 ACGTACGCTCGGTTG 32
 RESULT 15
 AC103862/c
 ID AC103862 standard; DNA; 25 BP.
 XX
 AC AC103862;
 XX
 DT 13-OCT-2003 (first entry)
 XX
 Human microarray DNA oligonucleotide SEQ ID NO 3853.
 DE
 KW EST ss; probe; expressed sequence tag; microarray; gene expression;
 KW genetic variation; biallelic marker; polymorphism; human;
 KW cross-species comparison.
 OS Homo sapiens.
 PN US2003104410-A1.
 XX
 PD 05-JUN-2003.
 XX
 PF 15-MAR-2002; 2002US-00098263.
 XX
 PR 16-MAR-2001; 2001US-0276759P.
 XX
 PA (AFFY-) AFFINMETRIX INC.
 XX
 PI Mittmann MP;
 XX
 DR WPI; 2003-567953/53.
 XX
 PT New array of nucleic acid probes, useful for in situ hybridization, in
 PT Southern, Northern or dot-blot hybridization to identify or detect the
 PT sequence or specific mutations of any gene.
 XX
 PS Claim 1; SEQ ID NO 3853; 9pp; English.
 XX
 The invention discloses a microarray comprising a plurality of nucleic
 CC acid probes including one of 2,018,500 fully defined sequences, or its
 CC perfect match, perfect mismatch, antisense match or antisense mismatch.
 CC Also disclosed is a method of gene expression analysis. The array is used
 PS

XX
 The invention relates to a method of decreasing the amount of N-terminal
 CC methionine methylation on a protein expressed in a bacterium. The
 CC bacterial methionine transferase which directs N-terminal methionine
 CC methylation recognises proteins which have a proline residue at position
 CC 4 (e.g., the bacterial ribosomal protein L16 and the bacterial chemotaxis
 CC protein cheZ). The method comprises introducing mutations into the DNA
 CC encoding the protein so that residue 4 is a non-proline residue, thereby
 CC reducing the degree of N-terminal methylation when the protein is
 CC expressed in a bacterium. The method is useful for decreasing methylation
 CC of a protein, particularly a recombinantly produced protein. The
 CC demethylated protein can be used in a pharmaceutical composition for the
 CC treatment of a disease but with less likelihood of eliciting an
 CC immunological response. These demethylated proteins may be used as
 CC therapeutic agent for the treatment and/or amelioration of disease or
 CC symptoms associated with a disease. The exemplifications describe the
 CC expression of a recombinant human haemoglobin construct (rhb1.1) in
 CC Escherichia coli, and its modification such that residue 4 of the di-
 CC alpha chain of the recombinant haemoglobin is altered from proline to a
 CC non-proline residue. The present sequence represents a PCR primer used in
 CC the exemplifications of the invention
 XX
 Sequence 42 BP; 3 A; 12 C; 16 G; 11 T; 0 U; 0 Other;
 SQ
 Query Match 69.0%; Score 13.8%; DB 5; Length 42;
 Best Local Similarity 88.2%; Pred. No. 8.3e+03;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 ACGGCGCGCTGGTCA 20
 Db 16 ACGTACGCTCGGTTG 32

RESULT 14
 AAC81485
 ID AAC81485 standard; DNA; 42 BP.
 XX
 AC AAC81485;
 XX
 DT 28-FEB-2001 (first entry)
 XX
 PBR322 ori downstream PCR primer, SEQ ID NO:21.
 DE
 Recombinant human haemoglobin; rhb1.1; bacterial expression;
 KW N-terminal methionine methylation signal; demethylation;
 KW Escherichia coli; non-immunogenic; pharmaceutical composition;
 KW PCR primer; ss.
 XX
 Synthetic.
 XX
 PN US6140071-A.
 XX
 PD 31-OCT-2000.
 XX
 PR 27-JAN-1994; 94US-00188374.
 XX
 PR 27-JAN-1994; 94US-00188374.
 XX
 PA (SOMA-) SOMATOGEN INC.
 XX
 PI Aitken JF, Apostol IZ, Levine JD, Lippincott JA;
 DR WPI; 2001-048957/06.
 XX
 Decreasing methylation of an N-terminal protein, especially haemoglobin
 PT having proline at amino acid position 4, useful for producing
 PT demethylated proteins for treating diseases, by altering this amino acid
 PT to a non-proline residue.
 XX
 Example 1; Col 15; 26pp; English.

CC in monitoring gene expression levels by hybridisation to a DNA library,
CC in analysis of genetic variation or in hybridisation of tag-labelled
CC compounds. The nucleic acid probes are specifically designed for analysis
CC of at least one target sequence. The method of analysis comprises
CC hybridising at least one or more nucleic acids to at least two or more
CC nucleic acid probes and detecting the hybridisation. The nucleic acid
CC probes are attached to a solid support. The analysis comprises monitoring
CC gene expression levels, identifying biallelic markers or polymorphisms,
CC or family members of a gene and a cross-species comparison. Each of the
CC nucleic acids further comprises a tag sequence. The array of nucleic acid
CC probes is useful in *in situ* hybridisation, in Southern, Northern or dot-
CC blot hybridisation to identify or detect the sequence or specific
CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
CC primer extensions or in screening cDNA or genomic libraries or subclones
CC for additional subclones containing segments of DNA that have been
CC isolated and previously sequenced. The sequence presented is one of the
CC nucleic acid probes incorporated in the microarray. Note: The sequence
CC data for this patent can also be obtained in the microarray. Note: The sequence
CC from USPTO at seqdata.uspto.gov/sequence.html.

XX
SQ Sequence 25 BP; 6 A; 8 C; 8 G; 3 T; 0 U; 0 Other;

Query Match 66.0%; Score 13.2; DB 9; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.6e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 GGACCGGGCGTCGGTCA 19
Db 24 GGACTCGTGGTCA 7

Search completed: December 13, 2005, 13:29:55
Job time : 263 Secs

Copyright (c) 1993 - 2005 Compugen Ltd.	GenCore version 5.1.6	AU104529 AU104529		
OM nucleic - nucleic search, using sw model		AU104530 AU104530		
Run on: December 13, 2005, 12:30:55 ; Search time 1918 Seconds	(without alignments)	AU105685 AU105685		
Title: US-10-605-498-82	487.874 Million cell updates/sec	AA765049 n278502.6		
Perfect score: 20		CC940970 01S0530-0		
Sequence: 1 gggacggcgccgtcggtcat 20		BH913356 326.1.39		
Scoring table: IDENTITY_NUC		CL639088 G0804708 G		
Gapop 10.0 , Gapext 1.0		CC183531 XB3344 Bay		
Searched: 41078325 seqs, 23393541228 residues		CL212525 G043F09 G		
Total number of hits satisfying chosen parameters: 179606		CL212525 AU103922		
Minimum DB seq length: 0		AU104465 AU104465		
Maximum DB seq length: 50		AU106742 AU106742		
Post-processing: Minimum Match 0%		CF296430 30DG5-06		
Maximum Match 100%		CL301794 P002A12 G		
Listing first 45 summaries				
Database : EST:*	RESULT 1			
1: gb_est1:*	BM050289	36 bp mRNA linear EST 07-NOV-2001		
2: gb_est2:*	LOCUS	603632006F1 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:5423352 5', mRNA sequence.		
3: gb_est3:*	DEFINITION			
4: gb_hic:*	ACCESSION	BM050289		
5: gb_est4:*	VERSION	BM050289.1 GI:16779556		
6: gb_est5:*	KEYWORDS	EST.		
7: gb_est6:*	SOURCE	Homo sapiens (human)		
8: gb_est7:*	ORGANISM	Homo sapiens		
9: gb_gss1:*		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae; Homo.		
10: gb_gss2:*	COMMENT	1 (bases 1 to 36) REFERENCE		
11: gb_gss3:*		NIH-MGC http://mgc.nci.nih.gov/.		
	AUTHORS	National Institutes of Health, Mammalian Gene Collection (MGC)		
	TITLE	Unpublished (1999)		
	JOURNAL			
	CONTACT	Email: cgabbs@mail.nih.gov		
	Tissue	Tissue Procurement: ATCC		
	Procurement	CDNA Library Preparation: Ling Hong/Rubin Laboratory		
	CDNA	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LiNL)		
	Sequencing	DNA Sequencing by: Incyte Genomics, Inc.		
		Clone: MGIC clone distribution information can be found through the I.M.A.G.E. Consortium/LiNL at: http://image.lnl.gov		
		Plate: LLCM1882 row: k column: 01		
		High quality sequence stop: 33.		
	FEATURES	Location/Qualifiers		
	source	1. .36 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone=IMAGE:5423352" /tissue_type="normal pigmented retinal epithelium" /lab_host="DH10B (phage-resistant)" /clone.lib="NIH MGC 43" /note="Organ: eye; Vector: pOTB7; Site_1: XbaI; Site_2: EcoRI; cDNA made by oligo-dN priming. Directionally cloned into EcoRI/XbaI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library. "		
Result No.	Query Score	Match Length	DB ID	Description
-	-	-	-	-
1	13.8	69.0	36 3	BM050289 603632506
2	13.6	68.0	49 7	C0780197 BL0094 A0
3	13.4	67.0	49 3	BT166726 60304726
4	12.8	66.0	37 2	BG166786 602339133
c	5	12.8	64.0	32 BP131807 601830724
c	6	12.8	64.0	B1553162 603197760
c	7	12.8	64.0	AU105403 AU105403
c	8	12.8	64.0	AU105404 AU105404
c	9	12.8	64.0	AU105405 AU105405
c	10	12.8	64.0	AU105406 AU105406
c	11	12.6	63.0	AU107987 AU107987
c	12	12.6	63.0	AU107995 AU107995
c	13	12.8	62.0	AG203073 Pan trogl
c	14	12.4	62.0	AU105647 AU105647
c	15	12.4	62.0	AU105649 AU105649
c	16	12.2	61.0	A1287864 qv07d12.x
c	17	12.2	61.0	BF525570 602039675
c	18	12.2	61.0	AQ026252 1(3)13130
c	19	12.2	61.0	AU107551 AU107551
c	20	12	60.0	AA867755 vx16008.x
c	21	12	60.0	CZ169504 G05C04 G
c	22	12	60.0	AI339668 qk63C12.x

ORIGIN	KEYWORDS	EST
Query Match 69.0%; Score 13.8; DB 3; Length 36; Best Local Similarity 88.2%; Pred. No. 8.6e+04; Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	SOURCE Homo sapiens (human) ORGANISM Homo sapiens COMMENT Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.	Homo sapiens (human)
Qy 1 GGGAGGGGGGGCTCGGT 17 Db 19 GGGGGGGGGGGCTCGGT 35	REFERENCE 1 (bases 1 to 49) AUTHORS NIH-MGC http://mgc.ncbi.nih.gov/ TITLE National Institutes of Health, Mammalian Gene Collection (MGC) JOURNAL Unpublished (1999) COMMENT Contact: Robert Strausberg, Ph.D. Email: cgsapbs-r@mail.nih.gov Tissue Procurement: Life Technologies, Inc. CDNA Library Preparation: Life Technologies, Inc. DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM1162 row: C column: 07.	
RESULT 2 COT780197	FEATURES Location/Qualifiers	
LOCUS COT780197 49 bp mRNA linear EST 05-AUG-2004 DEFINITION BL009A A05 6-DAY Axolotl Tail Blastema (6DAXBL) Ambystoma mexicanum CDNA 5' similar to hypothetical protein, mRNA sequence.	SOURCE 1.49 /mol type="mRNA" /db_Xref="taxon:9606" /clone="IMAGE:5185086" /lab host="DH10B" /clone lib="NIH_MGC_116" /note="Organ: Pooled colon, kidney, stomach; Vector: PCMV-SPORT6; Site 1: NotI; Site 2: EcoRI (destroyed); RNA source anonymous pool of 3 colons, age 26 yo male, 49 yo female, 71 yo male colon; 46 yo male kidney, and pool of 2 stomachs, 62 yo male and 70 yo female. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NIH MGC Library."	
REFERENCE 1 (bases 1 to 49) AUTHORS Habermann, B., Eppelien, A.G., Herklotz, S., Volkmer, M., Schackert, H.K., Wiebe, G. and Tanaka, E.M., Penkile, K., Epperlein, H.H., Schackert, H.K., Wiebe, G. and Tanaka, E.M.	ORIGIN	
TITLE An Ambystoma mexicanum EST sequencing project: Analysis of 17,352 expressed sequence tags from embryonic and regenerating blastema cDNA libraries	Query Match 67.0%; Score 13.4; DB 3; Length 49; Best Local Similarity 93.3%; Pred. No. 1.3e+05; Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
JOURNAL Genome Biol. (2004) In press COMMENT Contact: Eiji M. Tanaka	Qy 4 ACCCGGCCTCGCTGC 18 Db 31 AAGGGGCGCTCGCTC 45	
ORGANISM Ambystoma mexicanum (axolotl)	RESULT 4	
ORGANISM Ambystoma mexicanum (axolotl)	DEFINITION BG166786 LOCUS 6023:9133P1 NIH_MGC_89 Homo sapiens cDNA clone IMAGE:446993 5', mRNA sequence.	
FEATURES SOURCE Homo sapiens (human)	ACCESSION BG166786 DEFINITION 6023:9133P1 NIH_MGC_89 Homo sapiens cDNA clone IMAGE:446993 5', mRNA sequence.	
LOCUS B1760726 37 bp mRNA linear EST 06-FEB-2001	VERSION BG166786 KEYWORDS EST ORGANISM Homo sapiens COMMENT 1 (bases 1 to 37) AUTHORS NIH-MGC http://mgc.ncbi.nih.gov/ TITLE National Institutes of Health, Mammalian Gene Collection (MGC) JOURNAL Unpublished (1999) COMMENT Contact: cgsapbs-r@mail.nih.gov Tissue Procurement: ATCC CDNA Library Preparation: Life Technologies, Inc. DNA Sequencing by: Incyte Genomics, Inc.	
DEFINITION CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)	Qy 1 GGACCGGGCTCGCTGAT 20 Db 7 GGGCGGGCTCGCTGAT 26	
ACCESSION B1760726	Qy 68.0%; Score 13.6; DB 7; Length 49; Best Local Similarity 80.0%; Pred. No. 1e+05; Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	
VERSION B1760726	DEFINITION B1760726 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5185086 5', mRNA sequence.	
DEFINITION B1760726	ACCESSION B1760726	
ACCESSION B1760726	VERSION B1760726	

Db	8	GAGACGGGAGGCTCGG	23
RESULT	7		
AUTHOR	AU105403/c	AU105403	50 bp mRNA linear EST 28-JAN-2004
LOCUS	AU105403 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone	AU105403 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone	50 bp mRNA linear EST 28-JAN-2004
DEFINITION	AU105403 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone mRNA sequence.	AU105403 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone mRNA sequence.	AU105403 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone mRNA sequence.
ACCESSION	AU105403	AU105403	AU105403
VERSION	AU105403.1	GI:13554924	GI:13554924
SOURCE	Homo sapiens (human)	Homo sapiens (human)	Homo sapiens (human)
ORGANISM	Mammalia; Eutheria; Euarchontoglires; Primates; Catarhini; Hominidae; Homo.	Mammalia; Eutheria; Euarchontoglires; Primates; Catarhini; Hominidae; Homo.	Mammalia; Eutheria; Euarchontoglires; Primates; Catarhini; Hominidae; Homo.
FEATURES	source	ORIGIN	FEATURES
	1. .50 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="HRCL0340" /clone_lib="Sugano Homo sapiens cDNA library"	Query Match 64.0%; Score 12.8; DB 1; Length 50; Best Local Similarity 87.5%; Pred. No. 2.3e+5; Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0; /clone="HRCL0340" /clone_lib="Sugano Homo sapiens cDNA library"	source
COMMENT	Context: Yutaka Suzuki Department of Virology, University of Tokyo Institute of Medical Science, University of Tokyo 4-6-1, Shirokanedai, Minato-ku, Tokyo 108-8639, Japan Email: yusuzki@ims.u-tokyo.ac.jp	Query Match 64.0%; Score 12.8; DB 1; Length 50; Best Local Similarity 87.5%; Pred. No. 2.3e+5; Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0; /clone="HRCL0340" /clone_lib="Sugano Homo sapiens cDNA library"	source
REFERENCE	AUTHORS	RESULT	9
AUTHOR	Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakai,Y., Nakamura,Y., Suyama,A. and Sugano,S.	AU105405/c LOCUS AU105405 Sugano Homo sapiens 50 bp mRNA cDNA library Homo sapiens cDNA clone	AU105405 Sugano Homo sapiens 50 bp mRNA cDNA library Homo sapiens cDNA clone
TITLE	Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites	DEFINITION AU105405	DEFINITION AU105405
JOURNAL	EMBO Rep. 2 (5), 388-393 (2001)	ACCESSION AU105405.1	ACCESSION AU105405.1
PUBLMED	11375929	VERSION GI:13554926	VERSION GI:13554926
KEYWORDS		KEYWORDS EST.	KEYWORDS EST.
COMMENT		SOURCE Homo sapiens (human)	SOURCE Homo sapiens (human)
REFERENCE	AUTHORS	ORGANISM Homo sapiens	ORGANISM Homo sapiens
AUTHOR	Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakai,Y., Nakamura,Y., Suyama,A. and Sugano,S.	ORGANISM Homo sapiens	ORGANISM Homo sapiens
TITLE	Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites	TITLE	TITLE
JOURNAL	EMBO Rep. 2 (5), 388-393 (2001)	JOURNAL EMBO Rep. 2 (5), 388-393 (2001)	JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
PUBLMED	11375929	PUBMED 11375929	PUBMED 11375929
COMMENT		COMMENT Contact: Yutaka Suzuki	COMMENT Contact: Yutaka Suzuki
REFERENCE	AUTHORS	ORGANISM Homo sapiens	ORGANISM Homo sapiens
AUTHOR	Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakai,Y., Nakamura,Y., Suyama,A. and Sugano,S.	ORGANISM Homo sapiens	ORGANISM Homo sapiens
TITLE	Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites	TITLE	TITLE
JOURNAL	EMBO Rep. 2 (5), 388-393 (2001)	JOURNAL EMBO Rep. 2 (5), 388-393 (2001)	JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
PUBLMED	11375929	PUBMED 11375929	PUBMED 11375929
COMMENT		COMMENT Contact: Yutaka Suzuki	COMMENT Contact: Yutaka Suzuki
REFERENCE	AUTHORS	ORGANISM Homo sapiens	ORGANISM Homo sapiens
AUTHOR	Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakai,Y., Nakamura,Y., Suyama,A. and Sugano,S.	ORGANISM Homo sapiens	ORGANISM Homo sapiens
TITLE	Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites	TITLE	TITLE
JOURNAL	EMBO Rep. 2 (5), 388-393 (2001)	JOURNAL EMBO Rep. 2 (5), 388-393 (2001)	JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
PUBLMED	11375929	PUBMED 11375929	PUBMED 11375929

AG203073	AG203073	Pan troglodytes DNA, clone: RP43-087B01.T7, genomic survey sequence.	26 bp DNA, linear	GSS 06-MAR-2004	JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
DEFINITION	DEFINITION			mapping of mRNA start sites	
ACCESSION	ACCESSION			11375929	
VERSION	VERSION			Comment	
KEYWORDS	KEYWORDS	Pan troglodytes (chimpanzee)		Contact: Yutaka Suzuki	
SOURCE	SOURCE	Pan troglodytes		Department of Virology	
ORGANISM	ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Pan.		Institute of Medical Science, University of Tokyo	
REFERENCE	REFERENCE	1. Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J., Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, N. and Yoo, H. BAC end sequences of Library RP-43		4-6-1, Shirokanedai, Minato-ku, Tokyo 108-8639, Japan	
AUTHORS	AUTHORS			Email: yuszuki@ims.u-tokyo.ac.jp	
JOURNAL	JOURNAL			Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano, S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).	
REFERENCE	REFERENCE	2 (bases 1 to 26)		149-156 (1997).	
AUTHORS	AUTHORS	Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J., Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, N. and Yoo, H. Direct Submission		Location/Qualifiers	
JOURNAL	JOURNAL	Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of Bioscience and Biotechnology (RIBB), Genome Research Center (GRC); 52 Oun-dong, Yusong-gu, Daejon 305-333, Korea (E-mail: redstone@mail.ribb.re.kr, URL: http://phs.grc.ribb.re.kr/ , Tel: 82-42-866-7181, Fax: 82-42-860-4409)		1. .50 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone_lib="Sugano Homo sapiens cDNA library"	
COMMENT	COMMENT	Clones are derived from the chimpanzee BAC library RP-43. This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.		FEATURES	
PRIMERS	PRIMERS	Sequencing: T7		source	
LIBRARY	LIBRARY	Vector : pBACe3.6		Query Match	
		R.Site 1 : EcoRI		Best Local Similarity 92.0%	Score 12.4; DB 1;
		R.Site 2 : EcoRI.		Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	Length 50;
FEATURES	FEATURES	Location/Qualifiers		Qy	1 GGGACGGCGGCCTC 14
source	source	1.26 /organism="Pan troglodytes" /mol_type="genomic DNA" /db_xref="taxon:9598" /clone="RP43-087B01.T7" /sex="male" /cell_type="lymphocyte" /clone_lib="RP-43 Chimpanzee Male BAC Library"		Db	17 GGGAGCGGGCGCTC 4
ORIGIN	ORIGIN	Query Match		RESULT 15	
		Best Local Similarity 92.9%		AU105649/c	AU105649
		Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		DEFINITION	AU105649 Sugano Homo sapiens cDNA library
				ACCESSION	AU105649 HS10850, mRNA Sequence.
				VERSION	AU105649.1 GI:13555170 EST.
				KEYWORDS	Homo sapiens (human)
				ORGANISM	Homo sapiens
				REFERENCE	Metazoa; Chordata; Craniata; Vertebrata; Primates; Catarrhini; Hominidae; Homo.
				AUTHORS	1 (bases 1 to 50)
					Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
					Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
				JOURNAL	EMBO Rep. 2 (5), 388-393 (2001)
				PUBLISHED	11375929
				COMMENT	Contact: Yutaka Suzuki
					Department of Virology
					Institute of Medical Science, University of Tokyo
					4-6-1, Shirokanedai, Minato-ku, Tokyo 108-8639, Japan
					Email: yuszuki@ims.u-tokyo.ac.jp
					Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano, S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
RESULT 14	RESULT 14	Query Match		Location/Qualifiers	
AU105647/c	AU105647/c	Best Local Similarity 92.0%		1. .50 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606"	
DEFINITION	DEFINITION	Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		/clone="HS102850" /clone_lib="Sugano Homo sapiens cDNA library"	
ACCESSION	ACCESSION	Qy		ORIGIN	
VERSION	VERSION	1 GGGACGGCGGCCTC 14		Query Match	
KEYWORDS	KEYWORDS	Db		Best Local Similarity 92.9%	Score 12.4; DB 1;
SOURCE	SOURCE	1 GGGAGCGGGCGCTC 14		Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	Length 50;
ORGANISM	ORGANISM			Qy	1 GGGACGGCGGCCTC 14
REFERENCE	REFERENCE			Db	1 GGGAGCGGGCGCTC 14
AUTHORS	AUTHORS			RESULT 14	
				AU105647/c	AU105647
				DEFINITION	HS100961, mRNA Sequence.
				ACCESSION	AU105647 GI:13555168 EST.
				VERSION	Homo sapiens (human)
				KEYWORDS	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
				SOURCE	1 (bases 1 to 50)
				ORGANISM	Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
				REFERENCE	Diverse transcriptional initiation revealed by fine, large-scale
				AUTHORS	

Qy 1 GGGACGGCGGCCGCTC 14
Db 17 GTGACGGCGGCCGCTC 4

Search completed: December 13, 2005, 14:30:26
Job time : 1921 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
 Copyright (c) 1993 - 2005 Compugen Ltd.

1 nucleic - nucleic search, using sw model

run on: December 13, 2005, 13:16:54 ; Search time 94 Seconds
 (without alignment)

378.205 Million cell updates/sec

title: US-10-605-498-82

perfect score: 20

sequence: 1 9ggacggcgctcggtcat 20

scoring table: IDENTITY_NUC

Gapop 10_0 , Gapext 1.0

searched: 1303057 seqs, 888780828 residues

total number of hits satisfying chosen parameters: 1299706

RESULT 1
US-09-977-137A-16

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA: *

1: /seqn2_6_ptodata/1/ina/1_COMB.seq:*

2: /seqn2_6_ptodata/1/ina/5_COMB.seq:*

3: /seqn2_6_ptodata/1/ina/6A_COMB.seq:*

4: /seqn2_6_ptodata/1/ina/6B_COMB.seq:*

5: /seqn2_6_ptodata/1/ina/4_COMB.seq:*

6: /seqn2_6_ptodata/1/ina/PCTUS_COMB.seq:*

7: /seqn2_6_ptodata/1/ina/PP_COMB.seq:*

8: /seqn2_6_ptodata/1/ina/RE_COMB.seq:*

9: /seqn2_6_ptodata/1/ina/backfile.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14.2	71.0	33	3 US-09-977-137A-16	Sequence 16, Appl
2	2.1	70.0	25	3 US-09-396-196G-42173	Sequence 4623, A
3	13.8	69.0	25	3 US-09-396-196G-46323	Sequence 4623, A
4	13.8	69.0	25	3 US-09-396-196G-6324	Sequence 4624, A
5	13.8	69.0	25	3 US-09-396-196G-46335	Sequence 46335, A
6	13.8	69.0	42	2 US-09-153-071-14	Sequence 14, Appl
7	13.8	69.0	42	2 US-08-609-271-21	Sequence 21, Appl
8	13.8	69.0	42	2 US-08-438-511-14	Sequence 14, Appl
9	13.8	69.0	42	2 US-08-487-431-17	Sequence 17, Appl
10	13.8	69.0	42	3 US-08-188-374-21	Sequence 21, Appl
11	13.8	69.0	42	3 US-08-973-629-17	Sequence 17, Appl
12	13.2	66.0	25	3 US-09-396-533301	Sequence 53301, A
13	13	65.0	20	3 US-09-046-858A-19	Sequence 19, Appl
14	13	65.0	20	3 US-09-450-515-19	Sequence 19, Appl
15	13	65.0	20	3 US-10-206-654-19	Sequence 19, Appl
16	12.8	64.0	37	3 US-08-944-410-47	Sequence 47, Appl
17	12.8	64.0	40	2 US-08-425-684-86	Sequence 86, Appl
18	12.8	64.0	40	2 US-08-425-684-128	Sequence 128, Appl
19	12.8	64.0	40	2 US-08-675-502-16	Sequence 86, Appl
20	12.8	64.0	40	2 US-08-675-502-128	Sequence 128, Appl
21	12.8	64.0	40	3 US-09-245-802-96	Sequence 86, Appl
22	12.8	64.0	40	3 US-09-245-802-128	Sequence 128, Appl
23	12.6	63.0	20	3 US-10-131-827-8773	Sequence 15, Appl
24	12.6	63.0	20	3 US-09-540-014-25	Sequence 15, Appl
25	12.6	63.0	20	3 US-09-540-014-15	Sequence 15, Appl

GENERAL INFORMATION:
; Sequence 16, Application US/09977137A
; Patent No. 675042
; FILE REFERENCE: 79-00
; CURRENT APPLICATION NUMBER: US/09/977-137A
; CURRENT FILING DATE: 2001-10-12
; PRIORITY NUMBER: US 60/240,465
; PRIORITY FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO: 16
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; US-09-977-137A-16

Query Match 71.0%; Score 14.2%; DB 3; Length 33;
Best Local Similarity 84.2%; Pred. No. 3e-03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGAGCGGGCGCTGGTCA 19
Db 6 GGCTCTGGCGCTGGCA 24

RESULT 2
US-09-316-196G-42173/C
; Sequence 42173, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPICLANT: Michael Mittmann
; APPICLANT: David Lockhart
; APPICLANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/196,196G
; CURRENT FILING DATE: 1999-09-15
; PRIORITY NUMBER: 60/100,677
; PRIORITY FILING DATE: 2000-09-15

PRIOR FILING DATE: 1998-09-17
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 42173
 LENGTH: 25
 TYPE: DNA
 ORGANISM: Mus musculus
 US-09-396-196G-42173

Query Match 3 70.0%; Score 14; DB 3; Length 25;
 Best Local Similarity 100.0%; Pred. No. 3.8e+03;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 7 CGGCCCTCGGTCA 20
 Db 20 CGGCCCTCGGTCA 7

RESULT 3
 US-09-396-196G-46323/c
 Sequence 46323; Application US/09396196G
 Patent No 6821724
 GENERAL INFORMATION:
 APPLICANT: Michael Mittmann
 APPLICANT: David Mack
 APPLICANT: David Lockhart
 APPLICANT: Affymetrix, Inc.

TITLE OF INVENTION: Methods of Genetic Analysis
 CURRENT APPLICATION NUMBER: US/09/396,196G
 CURRENT FILING DATE: 1998-09-15
 PRIORITY NUMBER: 60/100,678
 PRIORITY FILING DATE: 1998-09-17
 NUMBER OF SEQ ID NOS: 122806
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 46323
 LENGTH: 25
 TYPE: DNA
 ORGANISM: mus musculus
 US-09-396-196G-46323

Query Match 3 69.0%; Score 13.8; DB 3; Length 25;
 Best Local Similarity 88.2%; Pred. No. 4.6e+03;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 4 ACGCGGGCTCGGGTCAT 20
 Db 20 ACGCTGCGACGGTCAT 4

RESULT 4
 US-09-396-196G-46324/c
 Sequence 46324; Application US/09396196G
 Patent No. 6821724
 GENERAL INFORMATION:
 APPLICANT: Michael Mittmann
 APPLICANT: David Mack
 APPLICANT: David Lockhart
 APPLICANT: Affymetrix, Inc.

TITLE OF INVENTION: Methods of Genetic Analysis
 FILE REFERENCE: 3101.1
 CURRENT APPLICATION NUMBER: US/09/396,196G
 CURRENT FILING DATE: 1998-09-15
 PRIORITY NUMBER: 60/100,678
 PRIORITY FILING DATE: 1998-09-17
 NUMBER OF SEQ ID NOS: 122806
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 46324
 LENGTH: 25
 TYPE: DNA
 ORGANISM: mus musculus
 US-09-396-196G-46324

Query Match 5 69.0%; Score 13.8; DB 3; Length 25;
 Best Local Similarity 88.2%; Pred. No. 4.6e+03;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 4 ACGGGGCTCGGTCA 20
 Db 19 ACGGTGGCACGTCAT 3

RESULT 5
 US-09-396-196G-46335/c
 Sequence 46335; Application US/09396196G
 Patent No. 682174
 GENERAL INFORMATION:
 APPLICANT: Michael Mittmann
 APPLICANT: David Mack
 APPLICANT: David Lockhart
 APPLICANT: Affymetrix, Inc.

TITLE OF INVENTION: Methods of Genetic Analysis
 CURRENT APPLICATION NUMBER: US/09/396,196G
 CURRENT FILING DATE: 1999-09-15
 PRIORITY NUMBER: 60/100,678
 PRIOR FILING DATE: 1998-09-17
 NUMBER OF SEQ ID NOS: 127806
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 46335
 LENGTH: 25
 TYPE: DNA
 ORGANISM: mus musculus
 US-09-396-196G-46335

Query Match 6 69.0%; Score 13.8; DB 3; Length 25;
 Best Local Similarity 88.2%; Pred. No. 4.6e+03;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 4 ACGGGGCTCGGTCA 20
 Db 18 ACGGTGGCACGTCAT 2

RESULT 6
 US-09-396-196G-46336/c
 Sequence 46336; Application US/09396196G
 Patent No. 682174
 GENERAL INFORMATION:
 APPLICANT: Ryland, James R.
 APPLICANT: Matthews, Maure-Ann H.
 APPLICANT: Houk, Daniel E.
 APPLICANT: Taylor, David W.
 APPLICANT: Williams, Lee R.
 APPLICANT: Mitchell, David J.
 APPLICANT: Chivers, Mark L.
 APPLICANT: Ernst, Ulrich P.
 APPLICANT: Belval, Thomas K.
 APPLICANT: Houk, Daniel E.
 APPLICANT: Taylor, David W.
 APPLICANT: Ryland, James R.
 APPLICANT: Matthews, Maure-Ann H.
 APPLICANT: Chivers, Mark L.
 APPLICANT: Ernst, Ulrich P.
 APPLICANT: Belval, Thomas K.
 TITLE OF INVENTION: Method for the Rapid Removal of
 PROTOPORPHYRIN IX from Protoporphyrin IX-Containing Solutions
 NUMBER OF SEQUENCES: 20
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Sonatogen, Inc.
 STREET: 5797 Central Avenue
 CITY: Boulder
 STATE: Colorado
 ZIP: 80301
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
 COMPUTER: Apple Macintosh
 OPERATING SYSTEM: System 7.0.1
 SOFTWARE: Microsoft Word 5.0a
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/153,071
 FILING DATE: No. 5665869ember 15, 1993
 CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:
 NAME: No. 5655869ak, Henry P.
 REGISTRATION NUMBER: 33200
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 303-541-3322
 TELEFAX: 303-444-3013
 INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 42
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: primer for pBR322 ori positions
 MOLECULE TYPE: 2380-2404
 HYPOTHETICAL: no
 US-01-153-071-14

RESULT 7
 US-01-609-271-21
 ; Sequence 21, Application US/08609271
 ; Patent No. 5611264
 ; GENERAL INFORMATION:
 ; APPLICANT: Aitken, Jacqueline F.
 ; APPLICANT: Apostol, Izzydor Z.
 ; APPLICANT: Lipincourt, Julie A.
 ; APPLICANT: Levine, Joseph D.
 ; TITLE OF INVENTION: Proteins with Mutations to Decrease N-Terminal Methylation
 ; NUMBER OF SEQUENCES: 42
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Somatogen, Inc.
 ; STREET: 2545 Central Avenue, Site FD-1
 ; CITY: Boulder
 ; STATE: Colorado
 ; ZIP: 80301

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
 COMPUTER: Apple Macintosh
 OPERATING SYSTEM: System 7.0.1
 SOFTWARE: Microsoft Word 5.0a
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/609,271
 FILING DATE: 28 February 1996
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/188,374
 FILING DATE: 1/27/94
 ATTORNEY/AGENT INFORMATION:
 NAME: No. 5611264ell1, Marianne F.
 REGISTRATION NUMBER: 38571
 NAME: Brown, Theresa A.
 REGISTRATION NUMBER: 32547
 REFERENCE/DOCKET NUMBER: 170/div
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 303-541-3324
 TELEFAX: 303-444-3013
 INFORMATION FOR SEQ ID NO: 21:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 42
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: primer for pBR322 ori positions 2380-2404
 HYPOTHETICAL: no

US-08-609-271-21
 ; Sequence 14, Application US/08438511
 ; Patent No. 5840851
 ; GENERAL INFORMATION:
 ; APPLICANT: Plomer, J. Jeffrey
 ; APPLICANT: Ryland, James R.
 ; APPLICANT: Matthews, Maura-Ann H.
 ; APPLICANT: Taylor, David W.
 ; APPLICANT: Milne, Erin E.
 ; APPLICANT: Durfee, Steven L.
 ; APPLICANT: Mathews, Antony J.
 ; APPLICANT: Neway, Justin O.
 ; TITLE OF INVENTION: Purification of Hemoglobin
 ; NUMBER OF SEQUENCES: 20
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Somatogen, Inc.
 ; STREET: 2545 Central Avenue, Suite FD1
 ; CITY: Boulder
 ; STATE: Colorado
 ; ZIP: 80301

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
 COMPUTER: Apple Macintosh
 OPERATING SYSTEM: System 7.0.1
 SOFTWARE: Microsoft Word 5.0a
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/438,511
 FILING DATE: 10 May 1995
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/339,304
 FILING DATE: No. 5840851ember 14, 1994
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/097,273
 FILING DATE: July 23, 1993
 ATTORNEY/AGENT INFORMATION:
 NAME: 5840851ell1, Marianne F.
 REGISTRATION NUMBER: 38571
 REFERENCE/DOCKET NUMBER: 191
 ATTORNEY/AGENT INFORMATION:
 NAME: Brown, Theresa A.
 REGISTRATION NUMBER: 32,547
 REGISTRATION NUMBER: 38571
 REFERENCE/DOCKET NUMBER: 191
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 303-541-3324
 TELEFAX: 303-444-3013
 INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 42
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: primer for pBR322 ori positions 2380-2404
 HYPOTHETICAL: no

US-08-438-511-14
 ; Sequence 8, Application US-08438511
 ; Patent No. 5840851
 ; GENERAL INFORMATION:
 ; APPLICANT: Plomer, J. Jeffrey
 ; APPLICANT: Ryland, James R.
 ; APPLICANT: Matthews, Maura-Ann H.
 ; APPLICANT: Taylor, David W.
 ; APPLICANT: Milne, Erin E.
 ; APPLICANT: Durfee, Steven L.
 ; APPLICANT: Mathews, Antony J.
 ; APPLICANT: Neway, Justin O.
 ; TITLE OF INVENTION: Purification of Hemoglobin
 ; NUMBER OF SEQUENCES: 20
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Somatogen, Inc.
 ; STREET: 2545 Central Avenue, Suite FD1
 ; CITY: Boulder
 ; STATE: Colorado
 ; ZIP: 80301

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
 COMPUTER: Apple Macintosh
 OPERATING SYSTEM: System 7.0.1
 SOFTWARE: Microsoft Word 5.0a
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/438,511
 FILING DATE: 10 May 1995
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/339,304
 FILING DATE: No. 5840851ember 14, 1994
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/097,273
 FILING DATE: July 23, 1993
 ATTORNEY/AGENT INFORMATION:
 NAME: 5840851ell1, Marianne F.
 REGISTRATION NUMBER: 32,547
 REGISTRATION NUMBER: 38571
 REFERENCE/DOCKET NUMBER: 191
 ATTORNEY/AGENT INFORMATION:
 NAME: Brown, Theresa A.
 REGISTRATION NUMBER: 32,547
 REGISTRATION NUMBER: 38571
 REFERENCE/DOCKET NUMBER: 191
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 303-541-3324
 TELEFAX: 303-444-3013
 INFORMATION FOR SEQ ID NO: 21:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 42
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: primer for pBR322 ori positions 2380-2404
 HYPOTHETICAL: no

Query Match 69 0%; Score 13.8; DB 2; Length 42;
 Best Local Similarity 88.2%; Pred. No. 4.4e-03;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 ACGGCGCGCGGGCAT 20
 Db 16 ACGGCGCGCGGGCAT 32

RESULT 8
 US-08-438-511-14
 ; Sequence 14, Application US/08438511
 ; Patent No. 5840851
 ; GENERAL INFORMATION:
 ; APPLICANT: Plomer, J. Jeffrey
 ; APPLICANT: Ryland, James R.
 ; APPLICANT: Matthews, Maura-Ann H.
 ; APPLICANT: Taylor, David W.
 ; APPLICANT: Milne, Erin E.
 ; APPLICANT: Durfee, Steven L.
 ; APPLICANT: Mathews, Antony J.
 ; APPLICANT: Neway, Justin O.
 ; TITLE OF INVENTION: Purification of Hemoglobin
 ; NUMBER OF SEQUENCES: 20
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Somatogen, Inc.
 ; STREET: 2545 Central Avenue, Suite FD1
 ; CITY: Boulder
 ; STATE: Colorado
 ; ZIP: 80301

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
 COMPUTER: Apple Macintosh
 OPERATING SYSTEM: System 7.0.1
 SOFTWARE: Microsoft Word 5.0a
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/438,511
 FILING DATE: 10 May 1995
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/339,304
 FILING DATE: No. 5840851ember 14, 1994
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/097,273
 FILING DATE: July 23, 1993
 ATTORNEY/AGENT INFORMATION:
 NAME: 5840851ell1, Marianne F.
 REGISTRATION NUMBER: 32,547
 REGISTRATION NUMBER: 38571
 REFERENCE/DOCKET NUMBER: 191
 ATTORNEY/AGENT INFORMATION:
 NAME: Brown, Theresa A.
 REGISTRATION NUMBER: 32,547
 REGISTRATION NUMBER: 38571
 REFERENCE/DOCKET NUMBER: 191
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 303-541-3324
 TELEFAX: 303-444-3013
 INFORMATION FOR SEQ ID NO: 21:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 42
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: primer for pBR322 ori positions 2380-2404
 HYPOTHETICAL: no

Query Match 69 0%; Score 13.8; DB 2; Length 42;
 Best Local Similarity 88.2%; Pred. No. 4.4e-03;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 ACGGCGCGCGGGCAT 20

Db 16 ||||||| 16 ACGTGCGTCGGTGT 32

RESULT 9
US-08-487-431-17
; Sequence 17, Application US/08487431
; GENERAL INFORMATION:
; APPLICANT: Anderson, David C.
; APPLICANT: Mathews, Anthony J.
; APPLICANT: Trimble, Stephen P.
; APPLICANT: Anthony-Cahill, Spencer
; TITLE OF INVENTION: Modified Hemoglobin-like Compounds
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Somaticogen, Inc.
; STREET: 2545 Central Avenue, Suite FD1
; CITY: Boulder
; ZIP: 80301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: System 7.5
; SOFTWARE: Microsoft Word 5.0a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,431
; FILING DATE: June 7, 1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/240,712
; FILING DATE: No. 5844090ember 6, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Theresa A.
; REGISTRATION NUMBER: 32,547
; REFERENCE/DOCKET NUMBER: 61
; ATTORNEY/AGENT INFORMATION:
; NAME: Ramsey R. Stewart
; REGISTRATION NUMBER: 38,322
; REFERENCE/DOCKET NUMBER: 61
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 303-541-3356
; TELEFAX: 303-444-3013
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Primer for BDR322 ori positions 2380-2404
; HYPOTHETICAL: no
; US-08-487-431-17

Query Match 69.0%; Score 13.8; DB 2; Length 42;
Best Local Similarity 88.2%; Pred. No. 4.4e+03; Mismatches 2; Indels 0; Gaps 0;
Matches 15; Conservative 0; Gaps 0;

Qy 4 ACGGGGCGCTGGGTAT 20
Db 16 ACGCTGGCTGGTGT 32

RESULT 10
US-08-188-374-21
; Sequence 21, Application US/08188374B
; Patent No. 6140071
; GENERAL INFORMATION:
; APPLICANT: Aitken F., Jacqueline
; APPLICANT: Apostol, Izidor Z.
; APPLICANT: Lippincott, Julie A.
; APPLICANT: Levine, Joseph D.
; TITLE OF INVENTION: Proteins with Mutations to Decrease N-Terminal Meth

; FILE REFERENCE: BXTB 1953
; CURRENT APPLICATION NUMBER: US/08/188,374B
; NUMBER OF SEQ ID NOS: 42
; SEQ ID NO 21
; LENGTH: 42
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer for pb32 ori positions 2380-2404
; US-08-188-374-21

Query Match 69.0%; Score 13.8; DB 3; Length 42;
Best Local Similarity 88.2%; Pred. No. 4.4e+03; Mismatches 2; Indels 0; Gaps 0;
Matches 15; Conservative 0; Gaps 0;

Qy 4 ACGGGGCGCTGGGTAT 20
Db 16 ACGCTGGCTGGTGT 32

RESULT 11
US-08-973-629-17
; Sequence 17, Application US/08973629A
; Patent No. 6150506
; GENERAL INFORMATION:
; APPLICANT: Trimble, Stephen
; APPLICANT: Mathews, Anthony
; APPLICANT: Kerwin, Bruce
; APPLICANT: Marquardt, David
; APPLICANT: Anthony-Cahill, Spencer
; APPLICANT: Epp, Janice
; APPLICANT: Madril, Dominic
; APPLICANT: Anderson, David
; TITLE OF INVENTION: MODIFIED HEMOGLOBIN-LIKE COMPOUNDS AND METHODS OF
; FILE REFERENCE: BXTB 1948
; CURRENT APPLICATION NUMBER: US/08/973,629A
; CURRENT FILING DATE: 1998-08-24
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 42
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide or 3', primer for generation of
; OTHER INFORMATION: pb32 ori with Pmel site
; US-08-973-629-17

Query Match 69.0%; Score 13.8; DB 3; Length 42;
Best Local Similarity 88.2%; Pred. No. 4.4e+03; Mismatches 2; Indels 0; Gaps 0;
Matches 15; Conservative 0; Gaps 0;

Qy 4 ACGGGGCGCTGGGTAT 20
Db 16 ACGCTGGCTGGTGT 32

RESULT 12
US-09-396-196G-53301
; Sequence 53301, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1

```

// CURRENT APPLICATION NUMBER: US/09/396,196G
// CURRENT FILING DATE: 1999-09-15
// PRIORITY APPLICATION NUMBER: 60/100,678
// PRIORITY FILING DATE: 1998-09-17
// NUMBER OF SEQ ID NOS: 127806
// SOFTWARE: FastSEQ for Windows version 4.0
// SEQ ID NO 53301
// LENGTH: 25
// TYPE: DNA
// ORGANISM: mus musculus
// US-09-396-196G-53301

RESULT 13
US-09-046-858A-19
// Sequence 19, Application US/09046858A
// Patent No. 604673
// GENERAL INFORMATION:
// APPLICANT: Rodriguez, Raymond L.
// TITLE OF INVENTION: SUGAR-REGULATORY SEQUENCES
// TITLE OF INVENTION: IN ALPHA-AMYLASE GENES
// NUMBER OF SEQUENCES: 21
// CORRESPONDENCE ADDRESS:
// ADDRESSEE: Dehlinger & Associates
// STREET: PO Box 60850
// CITY: Palo Alto
// STATE: CA
// COUNTRY: USA
// ZIP: 94306
// COMPUTER READABLE FORM:
// MEDIUM TYPE: Diskette
// COMPUTER: IBM Compatible
// OPERATING SYSTEM: DOS
// SOFTWARE: FastSEQ for Windows Version 2.0
// CURRENT APPLICATION DATA:
// APPLICATION NUMBER: US/09/046,858A
// FILING DATE: 24-MAR-1998
// CLASSIFICATION: 800
// PRIOR APPLICATION DATA:
// APPLICATION NUMBER: 60/042,376
// FILING DATE: 24-MAR-1997
// ATTORNEY/AGENT INFORMATION:
// NAME: Dehlinger, Peter J.
// REGISTRATION NUMBER: 28,006
// REFERENCE DOCKET NUMBER: 2000-0456.30
// TELECOMMUNICATION INFORMATION:
// TELEPHONE: 650-324-0880
// TELEFAX: 650-324-0960
// TELEK:
// INFORMATION FOR SEQ ID NO: 19:
// SEQUENCE CHARACTERISTICS:
// LENGTH: 20 base pairs
// TYPE: nucleic acid
// STRANDEDNESS: single
// TOPOLOGY: linear
// US-09-046-858A-19

Query Match 65.0%; Score 13; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1e+04; Mismatches 0; Indels 0; Gaps 0;
Matches 13; Conservative 0; Gaps 0;

Qy 3 GACGGGGCTCG 15
Db 2 GACGGGGCTCG 14

```

COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/206,654
FILING DATE: 25-JUL-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/046,858A
FILING DATE: 24-MAR-1998
APPLICATION NUMBER: 60/042,376
FILING DATE: 24-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Delinger, Peter J.
REGISTRATION NUMBER: 28,006
REFERENCE/DOCKET NUMBER: 2000-0456.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
TELEFAX: 650-324-0860
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
us-10-206-654-19

Query Match 65.0%; Score 13; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 GACCGGGCCCTCG 15
Db 2 GACCGGGCCCTCG 14

Search completed: December 13, 2005, 14:32:05
Job time : 95 SECs


```

; CURRENT FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US 60/415,859
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US 60/463,952
; PRIOR FILING DATE: 2003-04-18
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 81
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-605-498-81

Query Match 100.0%; Score 20; DB 7; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.5.; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Gaps 0;

Qy 1 GGGACGGCGCGCTGGTCAT 20
Db 2 GGGACGGCGCGCTGGTCAT 21

RESULT 3
US-10-605-498-90/C
; Sequence 90, Application US/10505498
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Rocchi, Palma
; APPLICANT: Sinaevsky, Maxim
; TITLE OF INVENTION: Compositions and Methods for Treatment of Prostate and Other
; TITLE OF INVENTION: Cancers
; FILE REFERENCE: UBC P-031
; CURRENT APPLICATION NUMBER: US/10/605,498
; CURRENT FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US 60/415,859
; PRIOR FILING DATE: 2002-10-02
; NUMBER OF SEQ ID NOS: 91
; SEQ ID NO: 90
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-10-605-498-90

Query Match 95.0%; Score 19; DB 7; Length 19;
Best Local Similarity 100.0%; Pred. No. 17.; Mismatches 0; Indels 0; Gaps 0;
Matches 19; Conservative 0; Gaps 0;

Qy 2 GGAGCGGGCGCTCGGTCA 20
Db 19 GGACCCGGCGCTCGGTCA 1

RESULT 4
US-10-605-498-3
; Sequence 3, Application US/10605498
; Publication No. US20040127441A1
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Rocchi, Palma
; APPLICANT: Sinaevsky, Maxim
; TITLE OF INVENTION: Compositions and Methods for Treatment of Prostate and Other
; TITLE OF INVENTION: Cancers
; FILE REFERENCE: UBC P-031
; CURRENT APPLICATION NUMBER: US/10/605,498
; CURRENT FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US 60/415,859
; PRIOR FILING DATE: 2002-10-02
; NUMBER OF SEQ ID NOS: 91
; SEQ ID NO: 4
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-605-498-4

Query Match 75.0%; Score 15; DB 7; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0; ; APPLICANT: Blume, John
 Query 1 GGGACCGGCCCTCG 15 ; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
 Publication No. US/11036317 ; FILE REFERENCE: 3654.1
 Db 7 GGGACCGGCCCTCG 21 ; CURRENT APPLICATION NUMBER: US/11/036,317
 ; CURRENT FILING DATE: 2005-01-13
 ; PRIORITY APPLICATION NUMBER: US 60/536,639
 ; PRIORITY FILING DATE: 2004-01-13
 ; NUMBER OF SEQ ID NOS: 991174
 ; SOFTWARE: Microarray Probe Sequence Listing Generator v 1.1
 ; SEQ ID NO 330516
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Mus musculus
 US-11-036-317-330516

RESULT 7
 US-11-036-317-261850
 ; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
 ; FILE REFERENCE: 3654.1
 ; CURRENT APPLICATION NUMBER: US/11/036,317
 ; CURRENT FILING DATE: 2005-01-13
 ; PRIORITY APPLICATION NUMBER: US 60/536,639
 ; PRIORITY FILING DATE: 2004-01-13
 ; NUMBER OF SEQ ID NOS: 991174
 ; SOFTWARE: Microarray Probe Sequence Listing Generator v 1.1
 ; SEQ ID NO 261850
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Mus musculus
 US-11-036-317-261850

Query Match 71.0%; Score 14.2; DB 10; Length 25;
 Best Local Similarity 84.2%; Pred. No. 3.6e+03;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 ; APPLICANT: Williams, Alan
 ; PRIORITY APPLICATION NUMBER: US/11036317
 ; PRIORITY FILING DATE: 2005-01-13
 ; NUMBER OF SEQ ID NOS: 991174
 ; SOFTWARE: Microarray Probe Sequence Listing Generator v 1.1
 ; SEQ ID NO 332488
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Mus musculus
 US-11-036-317-332488

RESULT 10
 US-11-036-317-332488
 ; Sequence 332488, Application US/11036317
 ; Publication No. US20050214823A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Williams, Alan
 ; PRIORITY APPLICATION NUMBER: US/11036317
 ; PRIORITY FILING DATE: 2005-01-13
 ; NUMBER OF SEQ ID NOS: 991174
 ; SOFTWARE: Microarray Probe Sequence Listing Generator v 1.1
 ; SEQ ID NO 332488
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Mus musculus
 US-11-036-317-332488

RESULT 8
 US-11-036-317-269817
 ; Sequence 269817, Application US/11036317
 ; Publication No. US20050214823A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Williams, Alan
 ; PRIORITY APPLICATION NUMBER: US/11036317
 ; PRIORITY FILING DATE: 2005-01-13
 ; NUMBER OF SEQ ID NOS: 991174
 ; SOFTWARE: Microarray Probe Sequence Listing Generator v 1.1
 ; SEQ ID NO 269817
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Mus musculus
 US-11-036-317-269817

Query Match 71.0%; Score 14.2; DB 10; Length 25;
 Best Local Similarity 84.2%; Pred. No. 3.6e+03;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0; ; APPLICANT: Blume, John
 Query 1 GGGACCGGCCCTCG 19 ; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
 Db 3 GGGACCGGCCATCTGCCA 21 ; FILE REFERENCE: 3654.1
 ; CURRENT APPLICATION NUMBER: US/11/036,317
 ; CURRENT FILING DATE: 2005-01-13
 ; PRIORITY APPLICATION NUMBER: US 60/536,639
 ; PRIORITY FILING DATE: 2004-01-13
 ; NUMBER OF SEQ ID NOS: 991174
 ; SOFTWARE: Microarray Probe Sequence Listing Generator v 1.1
 ; SEQ ID NO 332488
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Mus musculus
 US-11-036-317-332488

RESULT 11
 US-11-036-317-364465
 ; Sequence 364465, Application US/11036317
 ; Publication No. US20050214823A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Williams, Alan
 ; PRIORITY APPLICATION NUMBER: US/11036317
 ; PRIORITY FILING DATE: 2005-01-13
 ; NUMBER OF SEQ ID NOS: 991174
 ; SOFTWARE: Microarray Probe Sequence Listing Generator v 1.1
 ; SEQ ID NO 364465
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Mus musculus
 US-11-036-317-364465

RESULT 9
 US-11-036-317-330516
 ; Sequence 330516, Application US/11036317
 ; Publication No. US20050214823A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Williams, Alan

US-11-036-317-364465

Query Match 71.0%; Score 14.2; DB 10; Length 25;
 Best Local Similarity 84.2%; Pred. No. 3.6e+03; Indels 0; Gaps 0;
 Matches 16; Conservative 0; Mismatches 3;
 Qy 1 GGGAGCGGGGGCTCGGTCA 19
 Db 4 GGGAGCGGGGGATCTGCCA 22

RESULT 12
 US-11-036-317-406575
 ; Sequence 406575, Application US/11036317
 ; Publication No. US20050214823A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Williams, Alan
 ; Blume, John
 ; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
 ; CURRENT APPLICATION NUMBER: US/11/036,317
 ; CURRENT FILING DATE: 2005-01-13
 ; PRIOR APPLICATION NUMBER: US 60/536,639
 ; PRIOR FILING DATE: 2004-01-13
 ; NUMBER OF SEQ ID NOS: 991174
 ; SOFTWARE: Microarray Probe Sequence Listing Generator v 1.1
 ; SEQ ID NO: 406575
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Mus musculus
 US-11-036-317-406575

Query Match 71.0%; Score 14.2; DB 10; Length 25;
 Best Local Similarity 84.2%; Pred. No. 3.6e+03; Indels 0; Gaps 0;
 Matches 16; Conservative 0; Mismatches 3;
 Qy 1 GGGAGCGGGGGCTCGGTCA 19
 Db 7 GGGAGGGGGCTCGGTCA 25

RESULT 13
 US-11-036-317-536426
 ; Sequence 536426, Application US/11036317
 ; Publication No. US20050214823A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Williams, Alan
 ; Blume, John
 ; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
 ; CURRENT APPLICATION NUMBER: US/11/036,317
 ; CURRENT FILING DATE: 2005-01-13
 ; PRIOR APPLICATION NUMBER: US 60/536,639
 ; PRIOR FILING DATE: 2004-01-13
 ; NUMBER OF SEQ ID NOS: 991174
 ; SOFTWARE: Microarray Probe Sequence Listing Generator v 1.1
 ; SEQ ID NO: 536426
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Mus musculus
 US-11-036-317-536426

Query Match 71.0%; Score 14.2; DB 10; Length 25;
 Best Local Similarity 84.2%; Pred. No. 3.6e+03; Indels 0; Gaps 0;
 Matches 16; Conservative 0; Mismatches 3;
 Qy 1 CGGACCCGGGGCTCGGTCA 19
 Db 7 GGGAGGGGGCTCGGTCA 25

RESULT 14
 US-11-036-317-536427
 ; Sequence 536427, Application US/11036317
 ; Publication No. US20050214823A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Williams, Alan
 ; Blume, John
 ; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
 ; CURRENT APPLICATION NUMBER: US/11/036,317
 ; CURRENT FILING DATE: 2005-01-13
 ; PRIOR APPLICATION NUMBER: US 60/536,639
 ; PRIOR FILING DATE: 2004-01-13
 ; NUMBER OF SEQ ID NOS: 991174
 ; SOFTWARE: Microarray Probe Sequence Listing Generator v 1.1
 ; SEQ ID NO: 536427
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Mus musculus
 US-11-036-317-536427

Query Match 71.0%; Score 14.2; DB 10; Length 25;
 Best Local Similarity 84.2%; Pred. No. 3.6e+03; Indels 0; Gaps 0;
 Matches 16; Conservative 0; Mismatches 3;
 Qy 1 GGGACGGGGCTCGGTCA 19
 Db 7 GGGAGGGGGCTCGGTCA 25

RESULT 15
 US-09-977-137A-16
 ; Sequence 16, Application US/09977137A
 ; Publication No. US20030104524A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Summers, Anne O.
 ; Caguilat, Jonathan
 ; Blume, John
 ; TITLE OF INVENTION: Recombinant Host Cells and Methods for Producing Recombinant Host Cells
 ; TITLE OF INVENTION: Recombinant Host Cells and Methods for Producing Recombinant Host Cells
 ; FILE REFERENCE: 79-00
 ; CURRENT APPLICATION NUMBER: US/09/977-137A
 ; CURRENT FILING DATE: 2001-10-12
 ; PRIOR APPLICATION NUMBER: US 60/465,465
 ; PRIOR FILING DATE: 2000-10-12
 ; NUMBER OF SEQ ID NOS: 18
 ; SEQ ID NO: 16
 ; LENGTH: 33
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: primer
 US-09-977-137A-16

Query Match 71.0%; Score 14.2; DB 3; Length 33;
 Best Local Similarity 84.2%; Pred. No. 3.6e+03; Indels 0; Gaps 0;
 Matches 16; Conservative 0; Mismatches 3;
 Qy 1 GGGACGGGGCTCGGTCA 19
 Db 6 GGGAGGGGGCTCGGTCA 24

Search completed: December 13, 2005, 14:39:40
 Job time : 446 secs

GenCore version 5.1.6
 Copyright (c) 1993 - 2005 Compugen Ltd.

CM nucleic - nucleic search, using SW model

Run on: December 13, 2005, 13:30:05 ; Search time 144 Seconds
 (without alignment)
 51.924 Million cell updates/sec

Title: US-10-605-498-82

Perfect score: 20

Sequence: 1_99gacgccccctcgat 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 332430 seqs, 186927314 residues

Total number of hits satisfying chosen parameters: 6638722

Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA New:
1: /cgn2_6/podata/2/pubpna/us09_new_pub_seq:
2: /cgn2_6/podata/2/pubpna/us05_new_pub_seq:
3: /cgn2_6/podata/2/pubpna/us07_new_pub_seq:
4: /cgn2_6/podata/2/pubpna/us06_new_pub_seq:
5: /cgn2_6/podata/2/pubpna/pct_new_pub_seq:
6: /cgn2_6/podata/2/pubpna/us10_new_pub_seq:
7: /cgn2_6/podata/2/pubpna/us11_new_pub_seq:
8: /cgn2_6/podata/2/pubpna/us11_new_pub_seq:
9: /cgn2_6/podata/2/pubpna/us11_new_pub_seq:
10: /cgn2_6/podata/2/pubpna/us05_new_pub_seq:
*Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution, and is derived by analysis of the total score distribution.

ALIGNMENTS

RESULT 1
US-11-101-244-1008030/c
; Sequence 1008030, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khorrova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIORITY APPLICATION NUMBER: 60/502,050
; PRIORITY FILING DATE: 2003-09-10
; PRIORITY APPLICATION NUMBER: 60/426,137
; PRIORITY FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1551911
; SOFTWARE: Proprietary
; SEQ ID NO: 1008030
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1008030

Query Match 64.0%; Score 12.8;
Best Local Similarity 87.5%; DB 8;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0

Qy 3 GACCGGGCCTCGGTC 18
Db 17 GATAGGGCCTCGGTC 2

RESULT 2
US-11-033-784-1008030/c
; Sequence 1008030, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khorrova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
c 1	12.8	64.0	19	8 US-11-101-244-1008030	Sequence 1008030,
c 2	12.8	64.0	19	9 US-11-083-784-1008030	Sequence 1008030,
c 3	12.6	63.0	19	8 US-11-101-244-899787	Sequence 899787,
c 4	12.6	63.0	19	9 US-11-083-784-899787	Sequence 899787,
c 5	12.4	62.0	32	6 US-10-939-294A-16099	Sequence 16099, A
c 6	12.2	61.0	22	7 US-11-176-795-58	Sequence 58, App1
c 7	12.2	61.0	22	7 US-11-176-795-62	Sequence 62, App1
c 8	12.2	61.0	32	6 US-10-939-294A-15630	Sequence 15630, A
c 9	12	60.0	19	8 US-11-101-244-877585	Sequence 877585,
c 10	12	60.0	19	9 US-11-083-784-877585	Sequence 877585,
c 11	12	60.0	27	7 US-11-075-046-4	Sequence 4, App1
c 12	12	60.0	32	7 US-11-075-046-30	Sequence 30, App1
c 13	11.8	59.0	19	8 US-11-101-244-367714	Sequence 367714,
c 14	11.8	59.0	19	8 US-11-101-244-367714	Sequence 367714,
c 15	11.8	59.0	19	8 US-11-101-244-385820	Sequence 385820,
c 16	11.8	59.0	19	8 US-11-101-244-475963	Sequence 475963,
c 17	11.8	59.0	19	8 US-11-101-244-1128971	Sequence 1128971,
c 18	11.8	59.0	19	8 US-11-101-244-1221629	Sequence 1221629,
c 19	11.8	59.0	19	9 US-11-083-784-367704	Sequence 367704,
c 20	11.8	59.0	19	9 US-11-083-784-367714	Sequence 367714,
c 21	11.8	59.0	19	9 US-11-083-784-385820	Sequence 385820,
c 22	11.8	59.0	19	9 US-11-083-784-475963	Sequence 475963,
c 23	11.8	59.0	19	9 US-11-083-784-1128971	Sequence 1128971,

; APPLICANT: Scaringe, Stephen
 ; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
 ; FILE REFERENCE: 13499US
 ; CURRENT APPLICATION NUMBER: US/11/083,784
 ; CURRENT FILING DATE: 2005-03-18
 ; PRIORITY NUMBER: US/10/714,333
 ; PRIORITY NUMBER: 2003-11-14
 ; PRIORITY NUMBER: 60/502,050
 ; PRIORITY NUMBER: 60/502,050
 ; PRIORITY NUMBER: 60/426,137
 ; PRIORITY NUMBER: 2002-11-14
 ; NUMBER OF SEQ ID NOS: 1591911
 ; SOFTWARE: Proprietary
 ; SEQ ID NO: 1008030
 ; LENGTH: 19
 ; TYPE: RNA
 ; ORGANISM: Homo sapiens
 US-11-083-784-1008030

Query Match 64.0%; Score 12.8; DB 9; Length 19;
 Best Local Similarity 87.5%; Pred. No. 3.4e+03; Indels 0; Gaps 0;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 3 GACGCGGCGCTCGGTC 18
 Db 17 GATGAGGCGCTCGGTC 2

4

RESULT 3

US-11-101-244-899787
 ; Sequence 899787, Application US/11101244
 ; Publication No. US20050246794A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dharmacon, Inc.
 ; APPLICANT: Khvorova, Anastasia
 ; APPLICANT: Reynolds, Devin
 ; APPLICANT: Leake, Devin
 ; APPLICANT: Marshall, William
 ; APPLICANT: Scaringe, Stephen
 ; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
 ; FILE REFERENCE: 13499US
 ; CURRENT APPLICATION NUMBER: US/11/101,244
 ; CURRENT FILING DATE: 2005-04-07
 ; PRIORITY NUMBER: 60/502,050
 ; PRIORITY NUMBER: 60/502,050
 ; PRIORITY NUMBER: 60/426,137
 ; PRIORITY NUMBER: 2002-11-14
 ; NUMBER OF SEQ ID NOS: 1591911
 ; SOFTWARE: Proprietary
 ; SEQ ID NO: 899787
 ; LENGTH: 19
 ; TYPE: RNA
 ; ORGANISM: Homo sapiens
 US-11-101-244-899787

4

Query Match 63.0%; Score 12.6; DB 8; Length 19;
 Best Local Similarity 63.2%; Pred. No. 4.2e+03; Indels 0; Gaps 0;
 Matches 12; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 Qy 2 GGACCGGGCGCTCGGTCA 20
 Db 1 GGAAACGGCGCUGGUCAU 19

5

RESULT 5
 US-10-319-294A-16099/C
 ; Sequence 16099, Application US/10939294A
 ; Publication No. US20050216417A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Barany, Francis
 ; APPLICANT: Turner, Daniel
 ; APPLICANT: Pingle, Maneesh
 ; APPLICANT: Pincas, Hanna
 ; TITLE OF INVENTION: Methods for identifying target nucleic acid molecules
 ; FILE REFERENCE: 19603/4121 (CRF D-2995-02)
 ; CURRENT APPLICATION NUMBER: US/10/939,294A
 ; CURRENT FILING DATE: 2004-09-10
 ; PRIORITY NUMBER: US 60/502/731
 ; PRIORITY NUMBER: US 60/502/731
 ; NUMBER OF SEQ ID NOS: 38895
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO: 16099
 ; LENGTH: 32
 ; TYPE: DNA
 ; ORGANISM: Artificial
 ; FEATURE:
 ; OTHER INFORMATION: oligonucleotide probe
 US-10-319-294A-16099

Query Match 63.0%; Score 12.6; DB 8; Length 19;
 Best Local Similarity 63.2%; Pred. No. 4.2e+03; Indels 0; Gaps 0;
 Matches 12; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 Qy 2 GGACCGGGCGCTCGGTCA 20
 Db 1 GGAAACGGCGCUGGUCAU 19

6

RESULT 6
 US-11-176-795-58/C
 ; Sequence 58, Application US/11176795
 ; Publication No. US2005025517A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Marmaro, Jeffrey M
 ; TITLE OF INVENTION: Method and Device for Multiplex Amplification System
 ; FILE REFERENCE: 1
 ; CURRENT APPLICATION NUMBER: US/11/176,795

RESULT 4
 US-11-083-784-899787
 ; Sequence 899787, Application US/11083784
 ; Publication No. US20050245475A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dharmacon, Inc.
 ; APPLICANT: Khvorova, Anastasia
 ; APPLICANT: Reynolds, Devin
 ; APPLICANT: Leake, Devin

CURRENT FILING DATE: 2005-07-07
 NUMBER OF SEQ ID NOS: 84
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 58
 LENGTH: 22
 TYPE: DNA
 ORGANISM: Coliform Bacteria
 US-11-176-795-58

Query Match 61.0%; Score 12.2%; DB 7; Length 22;
 Best Local Similarity 82.4%; Pred. No. 6e+03;
 Matches 14; Conservative 0; Mismatches 3;
 Indels 0; Gaps 0;

Qy 2 GGACGGCGGCGCTGGTC 18
 Db 19 GATGCGCGGCGGTC 3

RESULT 7
 US-11-176-795-62/c
 / Sequence 62, Application US/11176795
 / Publication No. US2005055517A1
 / GENERAL INFORMATION:
 / APPLICANT: Gerdes, John C
 / APPLICANT: Marmaro, Jeffrey M
 / TITLE OF INVENTION: Method and Device for Multiplex Amplification System
 / FILE REFERENCE: 1
 / CURRENT FILING DATE: 2005-07-07
 / NUMBER OF SEQ ID NOS: 84
 / SOFTWARE: PatentIn Ver. 2.1
 / SEQ ID NO: 62
 / LENGTH: 22
 / TYPE: DNA
 / ORGANISM: Coliform Bacteria
 US-11-176-795-62

Query Match 61.0%; Score 12.2%; DB 7; Length 22;
 Best Local Similarity 82.4%; Pred. No. 6e+03;
 Matches 14; Conservative 0; Mismatches 3;
 Indels 0; Gaps 0;

Qy 2 GGACGGCGGCGCTGGTC 18
 Db 19 GATGCGCGGCGGTC 3

RESULT 8
 US-10-939-294A-15630
 / Sequence 15630, Application US/10939294A
 / Publication No. US20050266417A1
 / GENERAL INFORMATION:
 / APPLICANT: Barany, Francis
 / APPLICANT: Turner, Daniel
 / APPLICANT: Pingle, Maneesh
 / APPLICANT: Pincas, Haima
 / TITLE OF INVENTION: Methods for identifying target nucleic acid molecules
 / FILE REFERENCE: 19603/4121 (CRP D-2995-02)
 / CURRENT FILING DATE: 2004-09-10
 / PRIOR APPLICATION NUMBER: US 60/502/731
 / PRIOR FILING DATE: 2003-09-12
 / NUMBER OF SEQ ID NOS: 38895
 / SOFTWARE: PatentIn version 3.3
 / SEQ ID NO: 15630
 / LENGTH: 32
 / TYPE: DNA
 / ORGANISM: Artificial
 / OTHER INFORMATION: oligonucleotide probe
 / FEATURE:
 / US-10-939-294A-15630

Query Match 61.0%; Score 12.2%; DB 6; Length 32;
 Best Local Similarity 82.4%; Pred. No. 5.7e+03;

Matches 14; Conservative 0; Mismatches 3;
 Indels 0; Gaps 0;

Qy 2 GGACGGCGGCGCTGGTC 18
 Db 8 GGACGGCGGCGCTGGTC 24

RESULT 9
 US-11-101-244-877585/c
 / Sequence 877585, Application US/11101244
 / Publication No. US20050245794A1
 / GENERAL INFORMATION:
 / APPLICANT: Dharmacon, Inc.
 / APPLICANT: Khvorrova, Anastasia
 / APPLICANT: Reynolds, Angela
 / APPLICANT: Leake, Devin
 / APPLICANT: Marshall, William
 / APPLICANT: Scaringe, Stephen
 / TITLE OF INVENTION: Functional and Hyperfunctional siRNA
 / FILE REFERENCE: 13490US
 / CURRENT APPLICATION NUMBER: US/11101244
 / CURRENT FILING DATE: 2005-04-07
 / PRIOR APPLICATION NUMBER: 60/502,050
 / PRIOR FILING DATE: 2003-09-10
 / PRIOR APPLICATION NUMBER: 60/426,137
 / PRIOR FILING DATE: 2002-11-14
 / NUMBER OF SEQ ID NOS: 15911
 / SOFTWARE: Proprietary
 / SEQ ID NO: 877585
 / LENGTH: 19
 / TYPE: RNA
 / ORGANISM: Homo sapiens
 US-11-101-244-877585

Query Match 60.0%; Score 12; DB 8; Length 19;
 Best Local Similarity 100.0%; Pred. No. 7.5e+03;
 Matches 12; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

Qy 9 GCGCGCGGTAT 20
 Db 15 GCGCTGGTAT 4

RESULT 10
 US-11-083-784-877585/c
 / Sequence 877585, Application US/11083784
 / Publication No. US20050245475A1
 / GENERAL INFORMATION:
 / APPLICANT: Dharmacon, Inc.
 / APPLICANT: Khvorrova, Anastasia
 / APPLICANT: Reynolds, Angela
 / APPLICANT: Leake, Devin
 / APPLICANT: Marshall, William
 / APPLICANT: Scaringe, Stephen
 / TITLE OF INVENTION: Functional and Hyperfunctional siRNA
 / FILE REFERENCE: 13490US
 / CURRENT APPLICATION NUMBER: US/11/083,784
 / CURRENT FILING DATE: 2005-03-18
 / PRIOR APPLICATION NUMBER: US/10/714,333
 / PRIOR FILING DATE: 2003-11-14
 / PRIOR APPLICATION NUMBER: 60/502,050
 / PRIOR FILING DATE: 2003-09-10
 / PRIOR APPLICATION NUMBER: 60/426,137
 / PRIOR FILING DATE: 2002-11-14
 / NUMBER OF SEQ ID NOS: 15911
 / SOFTWARE: Proprietary
 / SEQ ID NO: 877585
 / LENGTH: 19
 / TYPE: RNA
 / ORGANISM: Homo sapiens
 US-11-083-784-877585

Query Match 60.0%; Score 12; DB 9; Length 19;

Best Local Similarity 100.0%; Pred. No. 7.5e+03;
Matches 12; Conservative 0; Mismatches 0;
Indels 0; Gaps 0;

STREET: FOUR EMBARCADERO CENTER, SUITE 3400
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94111

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/11/075,046
FILING DATE: 07-MAR-2005

CLASSIFICATION:
PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US/11/075,046
FILING DATE: 03-Oct-2000

CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:

NAME: RICHARD F. TRECARIN
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-58631-4/RFT/NBC

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989

INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 base pairs

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

FEATURE:
NAME/KEY: CDS
LOCATION: 6..32

US-11-075-046-30

Query Match Score 12; DB 7; Length 32;
Best Local Similarity 75.0%; Pred. No. 6.9e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Db 25 GCGACGCCGCGCTGCTCAT 6

RESULT 13
US-11-101-244-367704/c
Sequence 367704, Application US/11101244
Publication No. US20050246794A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Khorrova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 134990US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 367704
LENGTH: 19
TYPE: RNA
ORGANISM: Homo sapiens

Query Match Score 12; DB 7; Length 27;
Best Local Similarity 75.0%; Pred. No. 7.1e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Db 20 GGGACGGGGCTGGCTCAT 1

RESULT 12
US-11-075-046-30/c
Sequence 30, Application US/11075046
Publication No. US2005026853A1
GENERAL INFORMATION:
APPLICANT: P. D. CHRISTIAN, K. H. J. GORDON and
T. N. HANZLIK
TITLE OF INVENTION: INSECT VIRUSES AND THEIR USES IN
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: DORSEY & WHITNEY LLP

Query Match Score 11.8; DB 8;
Best Local Similarity 86.7%; Pred. No. 9.1e+03; Length 19;

RESULT 14

Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 ACGCGCGCTGGTC 18

Db 16 ACACGGCGCTGGTC 2

Query Match Score 59.0%; DB 8; Length 19;

Best Local Similarity 86.7%; Pred. No. 9.1e+03; Mismatches 0; Indels 0; Gaps 0;

Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 ACGCGCGCTGGTC 18

Db 15 ACACGGCGCTGGTC 1

Query Match Score 59.0%; DB 8; Length 19;

Best Local Similarity 86.7%; Pred. No. 9.1e+03; Mismatches 0; Indels 0; Gaps 0;

Organism: Homo sapiens

RESULT 15

Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 ACGCGCGCTGGTC 18

Db 15 ACACGGCGCTGGTC 1

Query Match Score 59.0%; DB 8; Length 19;

Best Local Similarity 86.7%; Pred. No. 9.1e+03; Mismatches 0; Indels 0; Gaps 0;

Organism: Homo sapiens

Query Match Score 59.0%; DB 8; Length 19;

Best Local Similarity 86.7%; Pred. No. 9.1e+03; Mismatches 0; Indels 0; Gaps 0;

Organism: Homo sapiens

THIS PAGE BLANK (USPTO)